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SEARCH REQUEST FORM

Requestor's Name: Jeffrey E. Russel (571) 272-0769 (STIC)

Serial Number: ~~09/972,772~~ 09/972,772

Date: 4-2-2004 Phone: 571.272.0769 Art Unit: 1654

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Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevent citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevent claim(s).

Please search SEQ ID NO:16 (PXAXYHA) in the U.S. patent application sequence database (pending, published, issued) in Geneseq/Swissprot/PIR, and in STN. Please require any hits to have 20 or fewer residues.

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Number of Searches: _____

Number of Databases: 2

Search Site

_____ STIC

_____ CM-1

_____ Pre-S

Type of Search

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

_____ IG

✓ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

✓ Other CGN

PTO-1590 (8-90)

FILE 'REGISTRY' ENTERED AT 09:56:44 ON 05 APR 2004
L1 32 S P.A..HA/SQSP AND SQL=<20

FILE 'HCAPLUS' ENTERED AT 09:58:02 ON 05 APR 2004
L2 25 S L1

L2 ANSWER 1 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 11 Jul 2003
ACCESSION NUMBER: 2003:532836 HCAPLUS
DOCUMENT NUMBER: 139:97654
TITLE: Lysine labeling reagent and methods of use
INVENTOR(S): Peters, Eric C.; Brock, Ansgar; Ericson, Christer
PATENT ASSIGNEE(S): IRM LLC, Bermuda
SOURCE: PCT Int. Appl., 63 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003056299	A2	20030710	WO 2002-US35581	20021105
WO 2003056299	A3	20040226		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2003228700	A1	20031211	US 2002-289009	20021105

PRIORITY APPLN. INFO.: US 2001-332988P P 20011105
US 2002-385835P P 20020603
US 2002-410382P P 20020912

OTHER SOURCE(S): MARPAT 139:97654

AB The present invention provides compds. which are useful as multifunctional labels in proteomics studies. The labels of the present invention are both lysine-specific and increase the overall sequence coverage obtained in polypeptide mapping expts., by for example, increasing the ionization efficiencies of lysine-terminated tryptic fragments. In certain aspects, the labels of the present invention can be used to measure differential quantitation, as for example, deuterium(s) can easily be introduced during their synthesis. In one aspect, a C-terminal derivatized lysine biases the fragment ion intensities strongly toward C-terminal fragment ions, resulting in a highly simplified tandem mass spectrum. In further aspects, the number of lysine residues can be determined in a polypeptide. 2-Methoxy-4,5-dihydro-1H-imidazole and 2-methoxy-4,5-tetradeutero-1H-imidazole were prepared and used to label the lysine residues in myoglobin. The myoglobin was digested

with trypsin and the peptides were analyzed by MALDI mass spectrometry.

IT **557064-43-4 557064-44-5 557064-45-6**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence of tryptic peptides of horse myoglobin, derivatization and MALDI mass spectrometry in relation to; lysine-containing peptide labeling reagent and use in proteomics and mass spectrometry)

L2 ANSWER 2 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 30 Jun 2003
ACCESSION NUMBER: 2003:495202 HCAPLUS
DOCUMENT NUMBER: 139:163463
TITLE: Biopanning of endotoxin-specific phage displayed peptides
AUTHOR(S): Thomas, Celestine J.; Sharma, Shilpi; Kumar, Gyanendra; Visweswariah, Sandhya S.; Surolia, Avadhesha
CORPORATE SOURCE: Molecular Biophysics Unit, Indian Institute of Science, Bangalore, 560012, India
SOURCE: Biochemical and Biophysical Research Communications (2003), 307(1), 133-138
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Elsevier Science
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Systemic bacterial infections frequently lead to a plethora of symptoms termed "endotoxic shock" or "sepsis. " Characterized by hypotension, coagulation abnormalities, and multiple organ failure, treatment of sepsis still remains mostly supportive. Of the various exptl. therapeutic interventional strategies, neutralization of endotoxin by peptides or proteins is becoming popular recently. Hence, design of endotoxin binding peptides is gaining currency as their structural complexity and mode of recognition of endotoxin precludes mounting of resistance against them by the susceptible bacteria by genetic recombination, mutation, etc. Earlier work from our laboratory had shown that the amphiphilic cationic peptides are good ligands for endotoxin binding. In this study, we report the results of studies with the 12 selected lipid A binding phage displayed peptides by biopanning of a repertoire of a random pentadecapeptide library displayed on the filamentous M-13 phage. A comparison of the sequences revealed no consensus sequence between the 12 selected peptides suggesting that the lipid A binding motif is not sequence specific which is in accord with the sequence variation seen with the naturally occurring anti-microbial and/or endotoxin binding peptides. Thus, the flexibility of the peptides coupled with their plasticity in recognizing the lipid A moiety, explains their tight binding to endotoxin. At a structural level, asym. distribution of the charged polar residues on one face of the helix and non-polar residues on the opposite face appears to correlate with their activity.

IT **574743-62-7**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(biopanning of endotoxin-specific phage displayed peptides)

REFERENCE COUNT: 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 3 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 13 Jun 2003
ACCESSION NUMBER: 2003:455053 HCAPLUS
DOCUMENT NUMBER: 139:7179
TITLE: Preparation of compounds comprising a methionine aminopeptidase 2 (MetAP-2) inhibitory core coupled to a peptide for modulation of angiogenesis
INVENTOR(S): Olson, Gary L.; Self, Christopher; Lee, Lily; Cook, Charles Michael; Birktoft, Jens; Morgan, Barry; Arico-Muendel, Christopher C.
PATENT ASSIGNEE(S): Praecis Pharmaceuticals Inc., USA
SOURCE: U.S. Pat. Appl. Publ., 48 pp., Cont.-in-part of U.S. Ser. No. 1,945.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 4
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003109671	A1	20030612	US 2002-138935	20020502
US 6548477	B1	20030415	US 2000-704251	20001101
US 2002193298	A1	20021219	US 2001-972772	20011005
US 2002151493	A1	20021017	US 2001-1945	20011101
WO 2003092608	A2	20031113	WO 2003-US13623	20030502
WO 2003092608	A3	20040115		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.:
US 2000-704251 A2 20001101
US 2001-972772 A2 20011005
US 2001-1945 A2 20011101
US 2002-138935 A 20020502

OTHER SOURCE(S): MARPAT 139:7179

AB The invention provides angiogenesis inhibitor compds. A-W-CONR1-Xn-CR3R4-Z-P [A is a Met-AP-2 inhibitory core; W is O or NR2; R1, R2 are H or alkyl; X is alkylene or substituted alkylene; n is 0 or 1; R3, R4 are H, (un)substituted alkyl or (hetero)aryl; or CR3R4 is carbocyclic, heterocyclic, or alkylene; Z is CO or alkylene-CO and P is a peptide comprising 1 to about 100 amino acid residues attached at its amino terminus to Z or a group OR5 or NR6R7, where R5-R7 are H, alkyl, (un)substituted alkyl or

azacycloalkyl or NR6R7 is (un)substituted heterocyclyl; or Z is O, NR6 (R8 = H or alkyl), alkylene-O, or alkylene-NR8 and P is H, alkyl or a peptide consisting of 1 to about 100 amino acid residues attached at its carboxy terminus to Z] comprising a MetAP-2 inhibitory core coupled to a peptide, as well as pharmaceutical compns. comprising the angiogenesis inhibitor compds. Thus, (3R,4S,5S,6R)-5-methoxy-4-[(2R, 3R)-2-methyl-3-(3-methylbut-2-enyl)oxiranyl]-1-oxaspiro[2.5]oct-6-ylcarbonyl-L-valine Me ester, prepared by acylation of L-valine Me ester hydrochloride, showed IC50 = 4.7 nM for inhibition of MetAP-2.

IT **478412-67-8P 478412-68-9P**
RL: PNU (Preparation, unclassified); RCT (Reactant); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent); USES (Uses)
(preparation of peptide MetAP-2 inhibitory core derivs. for modulation of angiogenesis)

L2 ANSWER 4 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 09 May 2003
ACCESSION NUMBER: 2003:356176 HCAPLUS
DOCUMENT NUMBER: 138:348758
TITLE: Endothelial-cell binding peptides for diagnosis and therapy
INVENTOR(S): Gyuris, Jeno; Lamphere, Lou; Morris, Aaron J.; Tsaioun, Katherine
PATENT ASSIGNEE(S): GPC Biotech Inc., USA
SOURCE: PCT Int. Appl., 126 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003037172	A2	20030508	WO 2002-US35258	20021101
WO 2003037172	C2	20031211		
WO 2003037172	A3	20040205		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

US 2003166004	A1	20030904	US 2002-286457	20021101

PRIORITY APPLN. INFO.: US 2001-334822P P 20011101

AB The present invention relates to peptides and their derivs. which bind to endothelial cells and inhibit their proliferation in in vitro assays, e.g., also referred to herein as endothelial cell binding peptide (ECBP) or ECBP sequence. These compns. may be combined with a pharmaceutically acceptable excipient or carrier and

used to inhibit angiogenesis and angiogenesis-related diseases such as cancer, arthritis, macular degeneration, and diabetic retinopathy.

IT **518998-85-1**
RL: DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(endothelial-cell binding peptides for diagnosis and therapy of angiogenesis-related disorders)

L2 ANSWER 5 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 28 Mar 2003
ACCESSION NUMBER: 2003:242370 HCAPLUS
DOCUMENT NUMBER: 138:267686
TITLE: Purification of enzymes involved in coenzyme metabolism from pathogenic bacteria for characterization in development of targets for antibiotics
INVENTOR(S): Edwards, Aled; Dharamsi, Akil; Vedadi, Masoud; Alam, Muhammad Zahoor; Awrey, Donald; Beattie, Bryan; Canadien, Veronica; Domagala, Megan; Houston, Simon; Kanagarajah, Dhushy; Li, Qin; Necakov, Sasha; Nethery, Kathleen; Pinder, Benjamin; Sheldrick, Bay; Vallee, Francois; Viola, Cristina
PATENT ASSIGNEE(S): Affinium Pharmaceuticals, Inc., Can.
SOURCE: PCT Int. Appl., 256 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003025006	A2	20030327	WO 2002-CA1427	20020920
WO 2003025006	A3	20040219		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.:
US 2001-324115P P 20010921
US 2001-325337P P 20010927
US 2001-326321P P 20011001
US 2001-326378P P 20011001
US 2001-326820P P 20011003
US 2001-335702P P 20011025
US 2001-340536P P 20011026
US 2001-350907P P 20011029

AB Methods of purifying and characterizing enzymes that may play a role

in cofactor metabolism in pathogenic bacteria are described. The proteins may be useful as targets for antibiotics and methods for identifying regions of the proteins that may be targeted by drugs are described. The invention also provides biochem. and biophys. characteristics of those polypeptides.

IT **503535-18-0**
RL: PRP (Properties)
(unclaimed sequence; purification of enzymes involved in coenzyme metabolism from pathogenic bacteria for characterization in development of targets for antibiotics)

L2 ANSWER 6 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 20 Dec 2002
ACCESSION NUMBER: 2002:965105 HCAPLUS
DOCUMENT NUMBER: 138:33374
TITLE: Therapeutic agents and methods of use thereof for the modulation of angiogenesis
INVENTOR(S): Olson, Gary L.; Self, Christopher; Lee, Lily; Cook, Charles Michael; Birktoft, Jens
PATENT ASSIGNEE(S): Praecis Pharmaceuticals Inc., USA
SOURCE: U.S. Pat. Appl. Publ., 38 pp., Cont.-in-part of U. S. Ser. No. 704,251.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 4
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002193298	A1	20021219	US 2001-972772	20011005
US 6548477	B1	20030415	US 2000-704251	20001101
WO 2002042295	A2	20020530	WO 2001-US46086	20011101
WO 2002042295	A3	20030220		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
AU 2002039479	A5	20020603	AU 2002-39479	20011101
US 2002151493	A1	20021017	US 2001-1945	20011101
EP 1330447	A2	20030730	EP 2001-987241	20011101
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
US 2003109671	A1	20030612	US 2002-138935	20020502
NO 2003001978	A	20030611	NO 2003-1978	20030430

PRIORITY APPLN. INFO.:

US 2000-704251	A2	20001101
US 2001-972772	A	20011005
US 2001-1945	A2	20011101
WO 2001-US46086	W	20011101

OTHER SOURCE(S): MARPAT 138:33374

AB The present invention provides angiogenesis inhibitor compds. comprising a MetAP-2 (methionine aminopeptidase-2)-inhibitory fumagillin core coupled to a peptide, as well as pharmaceutical compns. comprising the angiogenesis inhibitor compds. and a pharmaceutically acceptable carrier. The present invention also provides methods of treating an angiogenic disease, e.g., cancer, in a subject by administering to the subject a therapeutically effective amount of one or more of the angiogenesis inhibitor compds. of the invention.

IT **478412-67-8P 478412-68-9P**
RL: PNU (Preparation, unclassified); RCT (Reactant); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent); USES (Uses)
(MetAP-2-inhibitory peptides for the modulation of angiogenesis)

L2 ANSWER 7 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 21 Oct 2002
ACCESSION NUMBER: 2002:798426 HCAPLUS
DOCUMENT NUMBER: 138:150397
TITLE: Peptidomics of the larval Drosophila melanogaster central nervous system
AUTHOR(S): Baggerman, Geert; Cerstiaens, Anja; De Loof, Arnold; Schoofs, Liliane
CORPORATE SOURCE: Laboratory of Developmental Physiology and Molecular Biology, Katholieke Universiteit Leuven, Louvain, B-3000, Belg.
SOURCE: Journal of Biological Chemistry (2002), 277(43), 40368-40374
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Neuropeptides regulate most, if not all, biol. processes in the animal kingdom, but only seven have been isolated and sequenced from Drosophila melanogaster. In analogy with the proteomics technol., where all proteins expressed in a cell or tissue are analyzed, the peptidomics approach aims at the simultaneous identification of the whole peptidome of a cell or tissue, i.e. all expressed peptides with their posttranslational modifications. Using nanoscale liquid chromatog. combined with tandem mass spectrometry and data base mining, we analyzed the peptidome of the larval Drosophila central nervous system at the amino acid sequence level. We were able to provide biochem. evidence for the presence of 28 neuropeptides using an extract of only 50 larval Drosophila central nervous systems. Eighteen of these peptides are encoded in previously cloned or annotated precursor genes, although not all of them were predicted correctly. Eleven of these peptides were never purified before. Eight other peptides are entirely novel and are encoded in five different, not yet annotated genes. This neuropeptide expression profiling study also opens perspectives for other eukaryotic model systems, for which genome projects are completed or in progress.

IT **495402-07-8P**
RL: BSU (Biological study, unclassified); PRP (Properties); PUR (Purification or recovery); BIOL (Biological study); PREP

(Preparation)
(neuropeptides of larval Drosophila melanogaster central nervous system)
REFERENCE COUNT: 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 8 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 25 Jun 2002
ACCESSION NUMBER: 2002:474815 HCAPLUS
DOCUMENT NUMBER: 137:321810
TITLE: The interaction of a peptide with a scrambled hydrophobic/hydrophilic sequence (Pro-Asp-Ala-Asp-Ala-His-Ala-His-Ala-His-Ala-Ala-Ala-His-Gly) (PADH) with DPPC model membranes: a DSC study
AUTHOR(S): Grasso, Domenico; Milardi, Danilo; La Rosa, Carmelo; Impellizzeri, Giuseppe; Pappalardo, Giuseppe
CORPORATE SOURCE: Dipartimento di Scienze Chimiche, Universita' di Catania, Catania, 95125, Italy
SOURCE: Thermochimica Acta (2002), 390(1-2), 73-78
CODEN: THACAS; ISSN: 0040-6031
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Depending on their hydrophobicity, peptides can interact differently with lipid membranes inducing dramatic modifications into their host systems. In the present paper, the interaction of a synthetic peptide with a scrambled hydrophobic/hydrophilic sequence (Pro-Asp-Ala-Asp-Ala-His-Ala-His-Ala-His-Ala-Ala-Ala-His-Gly) (PADH) with 1,2-dipalmitoyl-sn-glycero-3-phosphocholine (DPPC) model membranes has been investigated by differential scanning calorimetry (DSC), adopting three different exptl. approaches. In the first, the peptide is forced to be included into the hydrocarbon region of the lipid bilayer, by codissolving it with the lipid giving rise to mixed multilamellar vesicles-peptide systems; in the second, this system is passed through an extruder, thus producing large unilamellar vesicles-peptide systems; in the third, it is allowed to interact with the external surface of the membrane. The whole of the DSC results obtained have shown that the incorporation of the peptide into the lipid bilayer by means of the first method induces a decrease in the enthalpy of the gel-liquid crystal transition of the membrane and a shift of the transition to the lower temps., thus resembling, in spite of its prevalently hydrophilic nature, the behavior of transbilayer hydrophobic peptides. The extrusion of these systems creates unilamellar vesicles free of peptides but of smaller size as evidenced by the decreased cooperativity of the transition. The peptide, added externally to the DPPC model membrane, has no effect on the phase behavior of the bilayer. These findings suggest that the effect of the interaction of scrambled hydrophobic/hydrophilic peptides into lipid bilayers strongly affects the thermotropic behavior of the host membrane depending on the preparation method of the lipid/peptide systems. The whole of the results obtained in the present paper can be useful in approaching studies of bioactive peptides/lipids systems.

IT **214628-28-1**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(effect of scrambled hydrophobic/hydrophilic sequence-containing peptide on thermotropic behavior of DPPC model membranes)
REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 9 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 21 Jun 2002
ACCESSION NUMBER: 2002:466188 HCAPLUS
DOCUMENT NUMBER: 137:43263
TITLE: Mouse laminin α4 chain G domain heparin-binding sites and therapeutic uses
INVENTOR(S): Kitagawa, Yasuo; Shitara, Kenya; Ohki, Yuji
PATENT ASSIGNEE(S): Kyowa Hakko Kogyo Co., Ltd., Japan
SOURCE: PCT Int. Appl., 139 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002048349	A1	20020620	WO 2001-JP5976	20010710
WO 2002048349	C1	20020718		

W: CA, JP, US
PRIORITY APPLN. INFO.: JP 2000-376899 A 20001212

AB Fragments of laminin α4 chain G domain capable of binding to heparin, recombinant expression, and use in inhibiting cell binding to extracellular matrix, contact of cells with capillary vessels, growth of cancer, signal transduction of a heparin-binding signal transducing mol., cell proliferation, differentiation and survival of cells, are disclosed. Fusion proteins of this fragment with a peptide tag is claimed. G domains of the mouse laminin α1 and α4 chains consisting of its five subdomains LG1-LG5 were overexpressed in Chinese hamster ovary cells and purified by heparin chromatog. α1LG1-LG5 and α4LG1-LG5 eluted at NaCl concns. of 0.30 and 0.47 M, resp. In solid phase binding assays with immobilized heparin, half-maximal concns. of 14 (α1LG1-LG5) and 1.4 nM (α4LG1-LG5) were observed N-Glycan cleavage of α4LG1-LG5 did not affect affinity to heparin. The affinity of α4LG1-LG5 was significantly reduced upon denaturation with 8 M urea but could be recovered by removing urea. Chymotrypsin digestion of α4LG1-LG5 yielded high and low heparin affinity fragments containing either the α4LG4-LG5 or α4LG2-LG3 modules, resp. Trypsin digestion of heparin-bound α4LG1-LG5 yielded a high affinity fragment of about 190 residues corresponding to the α4LG4 module, indicating that the high affinity binding site is contained within α4LG4. Competition for heparin binding of synthetic peptides covering the α4LG4 region with complete α4LG1-LG5 suggests that the sequence AHGRL1521 is crucial for high affinity binding. Introduction of mutations H1518A or R1520A in glutathione

S-transferase fusion protein of the α4LG4 module produced in Escherichia coli markedly reduced heparin binding activity of the wild type. When compared with the known structure of α2LG5, this sequence corresponds to the turn connecting strands E and F of the 14-stranded β-sheet sandwich, which is opposite to the proposed binding sites for calcium ion, α-dystroglycan, and heparan sulfate. Wnt1 release from the cells and tumor growth inhibition by α4LG4 were observed Induction of angiogenesis and fat cells was also observed

IT **437767-29-8**
RL: PRP (Properties)
(unclaimed sequence; mouse laminin α4 chain G domain heparin-binding sites and therapeutic uses)

REFERENCE COUNT: 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 10 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 12 May 2002
ACCESSION NUMBER: 2002:353610 HCAPLUS
DOCUMENT NUMBER: 136:364964
TITLE: Genes encoding endothelial cell-specific protein ECSM1 and ECSM4 and their use in imaging, diagnosis and treatment of diseases associated with vascular endothelium
INVENTOR(S): Bicknell, Roy; Huminiecki, Lukasz
PATENT ASSIGNEE(S): Imperial Cancer Research Technology Limited, UK
SOURCE: PCT Int. Appl., 248 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002036771	A2	20020510	WO 2001-GB4906	20011106
WO 2002036771	A3	20020906		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
AU 2002023784	A5	20020515	AU 2002-23784	20011106
EP 1334194	A2	20030813	EP 2001-992777	20011106
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				

PRIORITY APPLN. INFO.:
US 2000-245566P P 20001106
US 2001-273662P P 20010307
WO 2001-GB4906 W 20011106

Searcher : Shears 571-272-2528

AB The present invention relates to endothelial cell-specific genes and encoded polypeptides and materials and uses thereof in the imaging, diagnosis, and treatment of conditions involving the vascular endothelium. Two independent strategies for differential expression anal. were combined with exptl. verification to identify genes specifically or preferentially expressed in vascular endothelium: (1) EST cluster expression anal. in the human UniGene gene index, and (2) use of the data-mining tool SAGEmap xProfiler. Two highly endothelial-selective genes are provided and designated as endothelial cell-specific mol. 1 (ECSM1) and magic roundabout (endothelial cell-specific mols. 4; ECSM4). ECSM4 shows similar endothelial cell specificity to the marker currently accepted in the art as the best endothelial cell marker (von Willibrand factor). ECSM1 has no protein or nucleotide homologs and is most likely to code for a small protein of 103 amino acids (the longest and most upstream open reading frame which was identified in the contig sequence). The human magic roundabout (ECSM4) cDNA clone has been previously identified (GenBank AK000805) and encodes a protein much larger than the 417 amino acids coded in the AK000805 clone since the ORF has no apparent up-stream limit. These endothelial cell-specific genes provides new pharmaceutical targets for imaging, diagnosing, and treating medical conditions involving the endothelium.

IT **422320-93-2**
RL: BUU (Biological use, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(peptide fragment; genes encoding endothelial cell-specific protein ECSM1 and ECSM4 and their use in imaging, diagnosis and treatment of diseases associated with vascular endothelium)

L2 ANSWER 11 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 11 Dec 2001
ACCESSION NUMBER: 2001:890675 HCAPLUS
DOCUMENT NUMBER: 136:163197
TITLE: DNA Hydrolysis and Oxidative Cleavage by Metal-Binding Peptides Tethered to Rhodium Intercalators
AUTHOR(S): Copeland, Kimberly D.; Fitzsimons, Marilena P.; Houser, Robert P.; Barton, Jacqueline K.
CORPORATE SOURCE: Division of Chemistry and Chemical Engineering, California Institute of Technology, Pasadena, CA, 91125, USA
SOURCE: Biochemistry (2002), 41(1), 343-356
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB With the goal of developing artificial nucleases for DNA hydrolysis, metal-coordinating peptides have been tethered to a DNA-intercalating rhodium complex to deliver metal ions to the sugar-phosphate backbone. The intercalator, [Rh(phi)2bpy']Cl3 [phi = 9,10-phenanthrenequinone diimine; bpy' = 4-(butyric acid)-4'-methyl-2,2'-bipyridine], provides DNA binding affinity, and a metal-binding peptide contributes reactivity. This strategy for DNA hydrolysis is a general one, and zinc(II)-promoted cleavage has been demonstrated for two widely different tethered metallopeptides.

An intercalator coupled with a de novo-designed α helix containing two histidine residues has been demonstrated to cleave both supercoiled plasmid and linear DNA substrates. Mutation of this peptide confirms that the two histidine residues are essential for Zn2+ binding and cleavage. Zinc(II)-promoted cleavage of supercoiled plasmid has also been demonstrated with an intercalator-peptide conjugate containing acidic residues and modeled after the active site of the BamHI endonuclease. Other redox-active metals, such as copper, have been delivered to DNA with our intercalator-peptide conjugates to effect oxidative chemical Copper cleavage expts. and photocleavage expts. with [Rh(phi)2bpy']3+ complement the hydrolysis studies and provide structural information about the interactions between the tethered metallopeptides and DNA. Variation of the rhodium intercalator was also explored, but with a mismatch-specific intercalator, no site-specific hydrolysis was found. These expts., in which the peptide, the metal cation, and the intercalator components of the conjugate are each varied, illustrate some of the issues involved in creating an artificial nuclease with DNA intercalators and metallopeptides.

IT **398148-67-9 398148-70-4**
RL: BSU (Biological study, unclassified); RCT (Reactant); BIOL (Biological study); RACT (Reactant or reagent)
(DNA hydrolysis and oxidative cleavage by metal-binding peptides tethered to rhodium intercalators)

REFERENCE COUNT: 71 THERE ARE 71 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 12 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 05 Oct 1998
ACCESSION NUMBER: 1998:625502 HCAPLUS
DOCUMENT NUMBER: 129:302879
TITLE: Synthesis, spectroscopic characterization, and metal ion interaction of a new α-helical peptide
AUTHOR(S): Impellizzeri, Giuseppe; Pappalardo, Giuseppe; Purrello, Roberto; Rizzarelli, Enrico; Santoro, Anna Maria
CORPORATE SOURCE: Dipartimento Scienze Chimiche, Universita Catania, Catania, 95125, Italy
SOURCE: Chemistry--A European Journal (1998), 4(9), 1791-1798
CODEN: CEUJED; ISSN: 0947-6539
PUBLISHER: Wiley-VCH Verlag GmbH
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A 15-mer model peptide, H-Pro-Asp-Ala-Asp-Ala-His-Ala-His-Ala-His-Ala-Ala-Ala-His-Gly-OH, was synthesized by the solid phase method. The solution structure of this peptide was investigated by CD and NMR spectroscopy. CD results indicated that the peptide adopts a helical conformation in the presence of 2,2,2-trifluoroethanol (TFE) and its helicity is influenced by pH. NMR studies, carried out in 1:1 H2O/TFE, allowed the sequence-specific assignment of the proton resonances to be made, in addition to a more precise location of the helical structure in the peptide sequence. The ability of different divalent metal ions (Cu2+, Ni2+) to induce an α-helix was also

investigated in aqueous solution by means of CD spectroscopy; the results obtained indicate that Ni2+ is able to promote the α-helical conformation at neutral pH. In contrast, the CD spectrum of the Cu2+-peptide complex does not show any indication of a helical conformation. The reasons for this behavior are proposed on the basis of ESR and UV/Vis data.

IT **214628-28-1P**
RL: PEP (Physical, engineering or chemical process); PRP (Properties); SPN (Synthetic preparation); PREP (Preparation); PROC (Process)
(preparation, spectroscopic characterization, and metal ion interaction of α-helical peptide)

REFERENCE COUNT: 75 THERE ARE 75 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 13 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 20 Aug 1997
ACCESSION NUMBER: 1997:531864 HCAPLUS
DOCUMENT NUMBER: 127:204167
TITLE: Intersite helper function of T cells specific for a protein epitope that is not recognized by antibodies
AUTHOR(S): Rosenberg, Jana S.; Atassi, M. Zouhair
CORPORATE SOURCE: Verna and Marrs McLean Department of Biochemistry, Baylor College of Medicine, Houston, TX, 77030, USA
SOURCE: Immunological Investigations (1997), 26(4), 473-489
CODEN: IMINEJ; ISSN: 0882-0139
PUBLISHER: Dekker
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Humoral responses to a protein require T-B cell communication for B cell activation by T cells. Previous studies from this laboratory have mapped the T and B cell recognition sites (epitopes) on sperm-whale myoglobin (Mb) and several other proteins. It was found that, five of six regions on Mb recognized by T cells are also recognized by B cells (i.e. antibodies). There is, however, one region (E6) residing within Mb residues 61-77, that is recognized only by T cells and to which no antibody (Ab) responses are detectable. To investigate the function of this exclusive T cell epitope, the authors established, from E6-primed BALB/c mice, an E6-specific T cell line (TE6) which comprised Th2-type cells. These T cells provided help in vitro to B cells from Mb-primed BALB/c mice and activated them to produce anti-Mb Abs of the IgM (58.2%) and IgG (41.8%) isotypes. The helper activity of TE6 cells was dependent on the concentration of the challenging Ag (intact Mb or peptide E6) in culture. Action of soluble factors released from E6-activated TE6 cells on BMb cells led to low production of anti-Mb Abs, suggesting that activation of the B cells was more dependent on their contact with T cells. Mapping of the epitope recognition of the anti-Mb Abs produced in vitro by BMb cells on activation by TE6 revealed that this activation was not general to all antigenic regions recognized by anti-Mb Abs in BALB/c mice. E6-specific T cells caused in vitro activation and differentiation of BMb cells into plasma cells that

secreted anti-Mb Abs directed, in decreasing order, against the following Mb regions: E4 (107-120) > E3 (87-100) > E1 (10-22). Little or no Ab responses could be detected against peptides E2 (50-62), E5 (141-153) and E6 (61-77). With B cells of peptide-primed BALB/c mice, TE6 cells activated strongly E4-, E3- or E1-, and only very slightly E2- or E6-, primed B cells to secrete Abs against the correlate peptide, but failed completely to activate E5-primed B cells. The results show that a protein T cell epitope, to which no Abs are detectable, plays an active role in B cell responses against other epitopes within the same protein.

IT **118024-72-9**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(T-cell-exclusive epitope role in B-cell response to immunodominant epitopes on same antigen)

L2 ANSWER 14 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 21 Mar 1997
ACCESSION NUMBER: 1997:188147 HCAPLUS
DOCUMENT NUMBER: 126:302757
TITLE: Folding propensities of peptide fragments of myoglobin
AUTHOR(S): Reymond, Martine T.; Merutka, Gene; Dyson, H. Jane; Wright, Peter E.
CORPORATE SOURCE: Dep. Molecular Biology & Skaggs Inst. Chem. Biology, Scripps Res. Inst., La Jolla, CA, 92037, USA
SOURCE: Protein Science (1997), 6(3), 706-716
CODEN: PRCIEI; ISSN: 0961-8368
PUBLISHER: Cambridge University Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Myoglobin has been studied extensively as a paradigm for protein folding. As part of an ongoing study of potential folding initiation sites in myoglobin, we have synthesized a series of peptides covering the entire sequence of sperm whale myoglobin. We report here on the conformational preferences of a series of peptides that cover the region from the A helix to the FG turn. Structural propensities were determined using CD and NMR spectroscopy in aqueous solution, trifluoroethanol, and methanol. Peptides corresponding to helical regions in the native protein, namely the B, C, D, and E helixes, populate the α region of (.vphi., ψ) space in water solution but show no measurable helix formation except in the presence of trifluoroethanol. The F-helix sequence has a much lower propensity to populate helical conformations even in TFE. Despite several attempts, we were not successful in synthesizing a peptide corresponding to the A-helix region that was soluble in water. A peptide termed the AB domain was constructed spanning the A- and B-helix sequences. The AB domain is not soluble in water, but shows extensive helix formation throughout the peptide when dissolved in methanol, with a break in the helix at a site close to the A-B helix junction in the intact folded myoglobin protein. With the exception of one local preference for a turn conformation stabilized by hydrophobic interactions, the peptides corresponding to turns in the folded protein do not measurably populate β-turn conformations

in water, and the addition of trifluoroethanol does not enhance the formation of either helical or turn structure. In contrast to the series of peptides described here, earlier studies of peptides from the GH region of myoglobin show a marked tendency to populate helical structures (H), nascent helical structures (G), or turn conformations (GH peptide) in water solution This region, together with the A-helix and part of the B-helix, has been shown to participate in an early folding intermediate. The complete anal. of conformational properties of isolated myoglobin peptides supports the hypothesis that spontaneous structure formation in local regions of the polypeptide may play an important role in the initiation of protein folding.

IT **189134-95-0**
RL: PEP (Physical, engineering or chemical process); PRP (Properties); PROC (Process)
(folding propensities of peptide fragments of myoglobin)

REFERENCE COUNT: 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 15 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 04 Sep 1993
ACCESSION NUMBER: 1993:490109 HCAPLUS
DOCUMENT NUMBER: 119:90109
TITLE: Novel thrombin-inhibiting protein from triatomid bug
INVENTOR(S): Friedrich, Thomas; Bialojan, Siegfried; Kroeger, Burkhard; Kuenast, Christoph
PATENT ASSIGNEE(S): BASF A.-G., Germany
SOURCE: Ger. Offen., 7 pp.
CODEN: GWXXBX
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
DE 4136513	A1	19930513	DE 1991-4136513	19911106
WO 9309232	A1	19930513	WO 1992-EP2450	19921027
W: CA, JP, US				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, SE				
EP 612349	A1	19940831	EP 1992-922434	19921027
EP 612349	B1	19970305		
R: AT, BE, CH, DE, DK, ES, FR, GB, IT, LI, NL, SE				
AT 149568	E	19970315	AT 1992-922434	19921027
ES 2097931	T3	19970416	ES 1992-922434	19921027
US 5523287	A	19960604	US 1994-211942	19940426
PRIORITY APPLN. INFO.:			DE 1991-4136513	19911106
			WO 1992-EP2450	19921027

AB A thrombin-inhibiting protein was isolated from a homogenate of last-instar Rhodnius prolixus larvae by Q-Sepharose chromatog., affinity chromatog. on immobilized thrombin, mono-Q chromatog., and reversed-phase HPLC. The protein had pI 3.7-4.7, mol. weight 12,000, and the N-terminal amino acid sequence Glu-Gly-Gly-Glu-Pro-Cys-Ala-Cys-Pro-His-Ala-Leu-His-Arg-Val-Cys-Gly-Ser-Asp. It may be produced

by recombinant DNA methodol. for use as an antithrombotic, in blood preservation, etc.

IT **149183-28-8**
RL: BIOL (Biological study)
(thrombin-inhibiting protein amino-terminal fragment of Rhodnius prolixus)

L2 ANSWER 16 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 26 Jun 1993
ACCESSION NUMBER: 1993:255311 HCAPLUS
DOCUMENT NUMBER: 118:255311
TITLE: Synthesis and circular dichroism spectra of sperm whale myoglobin-(57-96)-tetracontapeptide
AUTHOR(S): Hashimoto, Chikao; Muramatsu, Ichiro
CORPORATE SOURCE: Sch. Med., Jikei Univ., Tokyo, 182, Japan
SOURCE: Bulletin of the Chemical Society of Japan (1993), 66(1), 181-90
CODEN: BCSJA8; ISSN: 0009-2673
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A protected sperm whale myoglobin-(57-96)-tetracontapeptide was synthesized by successive condensations of Boc-(70-76)-OH (Boc = tert-butoxycarbonyl), Boc-(62-69)-OH, and Boc-(57-61)-OH fragments to partially protected ester H-(77-96)-OCH2Ph. After removal of the protecting groups, the crude product was purified with reversed-phase HPLC to yield sperm whale myoglobin-(57-96)-tetracontapeptide (I). The CD spectra showed that I was in a random conformation in 0.10 M phosphate buffer (pH 6.50) and in a 69% α-helix conformation in 60% 2,2,2-trifluoroethanol-0.10 M phosphate buffer (pH 6.50).

IT **126301-55-1**
RL: RCT (Reactant); RACT (Reactant or reagent)
(deblocking and peptide coupling reactions of, in preparation of myoglobin fragment)

L2 ANSWER 17 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 10 Jan 1993
ACCESSION NUMBER: 1993:11732 HCAPLUS
DOCUMENT NUMBER: 118:11732
TITLE: Fusion polypeptides prodrugs cleavable by dipeptidylpeptidase IV
INVENTOR(S): Kubiak, Teresa M.; Sharma, Satish K.
PATENT ASSIGNEE(S): Upjohn Co., USA
SOURCE: PCT Int. Appl., 54 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9210576	A1	19920625	WO 1991-US9152	19911212

W: AU, BB, BG, BR, CA, CS, FI, HU, JP, KP, KR, LK, MG, MN, MW, NO, PL, RO, SD, SU, US
RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR, GA, GB,

GN, GR, IT, LU, MC, ML, MR, NL, SE, SN, TD, TG

CA 2094512	AA	19920614	CA 1991-2094512	19911212
AU 9191165	A1	19920708	AU 1991-91165	19911212
AU 662508	B2	19950907		
EP 561971	A1	19930929	EP 1992-901817	19911212
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, MC, NL, SE				
JP 06503473	T2	19940421	JP 1992-501996	19911212
HU 69963	A2	19950928	HU 1993-1705	19911212
NO 9302148	A	19930809	NO 1993-2148	19930611
RU 2114119	C1	19980627	RU 1993-45577	19930611
PRIORITY APPLN. INFO.:			US 1990-626727	19901213
			WO 1991-US9152	19911212

OTHER SOURCE(S): MARPAT 118:11732

AB Nonnaturally occurring fusion polypeptides containing N-terminal extension peptide portions cleavable by dipeptidylpeptidase IV are disclosed which can be prepared recombinantly or by peptide synthesizer techniques. The fusion polypeptides are useful as prodrugs. Methods of affinity-purifying the desired active proteins are also disclosed. Bovine growth hormone-releasing factor (bGRF) analog [Leu27]bGRF(1-29)NH2 (I) was generated from 3 N-terminally-extended analogs: Tyr-Ala-Tyr-Ala-I, Ile-Ala-I (II), and Tyr-Ala-I upon incubation with bovine plasma in vitro. Moreover, the time at which I released from the prodrug was present correlated well with the prodrug extension length. When Holstein steers were injected i.v. with II at 0.2 nmol/kg body weight, plasma growth hormone levels were elevated to levels comparable to those generated upon i.v. injection with the same dose of I. As II had only .apprx.5% inherent potency of I, I must have been released from the extended peptide in vivo.

IT **144505-38-4**
RL: BIOL (Biological study)
(as dipeptidylpeptidase IV-cleavable extension peptide at amino-terminus of active core protein)

L2 ANSWER 18 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 23 Aug 1992
ACCESSION NUMBER: 1992:470320 HCAPLUS
DOCUMENT NUMBER: 117:70320
TITLE: Synthesis of sperm whale myoglobin-(77-96)-eicosapeptide and circular dichroism spectra of the related peptides
AUTHOR(S): Hashimoto, Chikao
CORPORATE SOURCE: Sch. Med., Jikei Univ., Chofu, 182, Japan
SOURCE: Bulletin of the Chemical Society of Japan (1992), 65(5), 1268-74
CODEN: BCSJA8; ISSN: 0009-2673
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Sperm whale myoglobin fragments (91-96) (I), (85-90) (II), (77-84) (III), (85-96) (IV), and (77-96) (V) peptides were prepared Protected precursors of I, II, and IV partly changed into pyroglutamic acid derivs. during deprotection and purification by various forms of column chromatog. The CD spectra of free peptides I-V in 0.10M phosphate buffers at pH 4.00, 6.50, and 8.50 were not typical of the helical structure. However, the CD spectra of peptides II, IV, and V in 60% 2,2,2-trifluoroethanol-0.10M phosphate buffers at the same pHs

showed profiles characteristic of a helical structure.

IT **126301-55-1**
RL: RCT (Reactant); RACT (Reactant or reagent)
(deblocking of, with hydrogen fluoride)

IT **126301-54-0**
RL: RCT (Reactant); RACT (Reactant or reagent)
(deblocking of, with methanesulfonic acid)

IT **142473-35-6P**
RL: FORM (Formation, nonpreparative); PREP (Preparation)
(formation of, in deblocking of protected glutamic acid derivative with methanesulfonic acid)

IT **142473-27-6P 142473-29-8P**
RL: PRP (Properties); SPN (Synthetic preparation); PREP (Preparation)
(preparation and conformation of, by CD)

L2 ANSWER 19 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 12 May 1990
ACCESSION NUMBER: 1990:179814 HCAPLUS
DOCUMENT NUMBER: 112:179814
TITLE: Synthesis of a protected sperm whale myoglobin-(77-96)-eicosapeptide and circular dichroism spectra of the related peptides
AUTHOR(S): Hashimoto, Chikao; Muramatsu, Ichiro
CORPORATE SOURCE: Sch. Med., Jikei Univ., Chofu, 182, Japan
SOURCE: Bulletin of the Chemical Society of Japan (1989), 62(6), 1900-7
CODEN: BCSJA8; ISSN: 0009-2673
DOCUMENT TYPE: Journal
LANGUAGE: English
OTHER SOURCE(S): CASREACT 112:179814
AB A protected sperm whale myoglobin-(77-96)-eicosapeptide (I) was synthesized by a solution method. The protected peptide I was purified by silica gel column chromatog. with BuOH-AcOH-H2O. The CD spectra of protected fragment peptides were measured in CF3CH2OH. A protected sperm whale myoglobin-(85-96)-dodecapeptide and I showed CD profiles characteristic of a helical structure.

IT **126301-55-1P**
RL: PRP (Properties); SPN (Synthetic preparation); PREP (Preparation)
(preparation and conformation of, by CD)

IT **126301-54-0P**
RL: SPN (Synthetic preparation); PREP (Preparation)
(preparation, peptide coupling of, with myoglobin octapeptide fragment, in conformation of, by CD)

L2 ANSWER 20 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 31 Mar 1990
ACCESSION NUMBER: 1990:116832 HCAPLUS
DOCUMENT NUMBER: 112:116832
TITLE: Antigen presentation by non-immune B-cell hybridoma clones: presentation of synthetic antigenic sites reveals clones that exhibit no specificity and clones that present only one epitope
AUTHOR(S): Cohly, Hari H. P.; Morrison, Dennis R.; Atassi,

M. Zouhair
CORPORATE SOURCE: Johnson Space Cent., NASA, Houston, TX, 77058, USA
SOURCE: Immunological Investigations (1989), 18(8), 987-92
CODEN: IMINEJ; ISSN: 0882-0139
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Recently, the authors reported the preparation and antigen-presenting properties of hybridoma B-cell clones obtained after fusing non-secreting, non-antigen presenting Balb/c 653-myeloma cells with non-immune SJL spleen cells. Here, specific and general presenter B cell clones were tested for their epitope presentation ability to SJL T-cells that were specific to lysozyme or myoglobin. B-cell clone A1G12, a general presenter which presented both lysozymes and myoglobin to their resp. T-cell lines, presented all 5 myoglobin epitopes while clone A1L16, a lysozyme-specific presenter, presented only 1 of the 3 epitopes of lysozyme. The latter reveals a hitherto unknown submol. specificity (to a given epitope within a protein) for antigen presenting cells at the clonal level. Therefore, the specificity of T-cell recognition does not only derive from the T-cell but may also be dependent on the epitope specificity of the antigen-presenting B-cell.

IT **88530-81-8**
RL: PROC (Process)
(presentation of, to T-cells, by non-immune B-cells, specificity of)

L2 ANSWER 21 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 21 Jan 1989
ACCESSION NUMBER: 1989:21983 HCAPLUS
DOCUMENT NUMBER: 110:21983
TITLE: T cell response to myoglobin: a comparison of T cell clones in high-responder and low-responder mice
AUTHOR(S): Gorai, Itsuo; Aihara, Michiko; Bixler, Garvin S., Jr.; Atassi, M. Zouhair; Walden, Peter; Klein, Jan
CORPORATE SOURCE: Abt. Immungenet., Max-Planck-Inst. Biol., Tuebingen, Fed. Rep. Ger.
SOURCE: European Journal of Immunology (1988), 18(9), 1329-35
CODEN: EJIMAF; ISSN: 0014-2980
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Mice carrying the H-2b haplotype (e.g., inbred strains C57BL/6 and C57BL/10) are low responders to sperm whale myoglobin when tested in the T cell proliferation assay. Their response is improved by the removal of the Ly-2+ cells from the lymph node population, but it still remains significantly lower than that of cells from high-responder strains (e.g., DBA/2, H-2d). To determine whether T cells from the low and high-responder mice recognize the same or different epitopes on the immunizing antigen, sets of T cell clones from both strains were tested against peptides representing different regions of the myoglobin mol., as well as against myoglobins from species other than the sperm whale. Four types of T cell clones were

obtained from the DBA/2 mice: 3 types responded to the peptide 107-120 (9 clones altogether), and 1 type responded to the peptide 133-149 (4 clones altogether). The 3 types responding to the peptide 107-120 could be distinguished by their response to horse myoglobin or by the restriction of the response (Ad vs. Ed). Similarly, 5 types of T cell clones were obtained from the C57BL/6 mice: 2 types responsed to the peptide 10-22 (1 type, but not the other, responded to horse myoglobin); 1 type responded to the peptide 133-149; and 2 types did not respond to any of the peptides used (1 type, but not the other, responded to dog myoglobin). All 5 types (13 clones altogether) were presumably Ab restricted. These results demonstrate the diversity of epitopes in single antigenic regions and show equivalent heterogeneity of T cell repertoires in high and low responder mice. Attempts to demonstrate specific T cell suppression in the low responder mice failed; only partial, nonspecific suppression was observed

IT **118024-72-9**
RL: BIOL (Biological study)
(of myoglobin, T-lymphocyte immune response to, H-2 haplotype in, of mouse)

L2 ANSWER 22 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 28 Oct 1988
ACCESSION NUMBER: 1988:545522 HCAPLUS
DOCUMENT NUMBER: 109:145522
TITLE: Prediction of peptide retention times
AUTHOR(S): Sakamoto, Yasuhiro; Kawakami, Nami; Sasagawa, Tatsuru
CORPORATE SOURCE: Sci. Instrum. Div., Tosoh Co., Ayase, 252, Japan
SOURCE: Journal of Chromatography (1988), 442, 69-79
CODEN: JOCRAM; ISSN: 0021-9673
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A new approach for predicting the retention times of peptides, either with isocratic or gradient elution is described. The isocratic capacity factors of peptides are correlated with their mol. wts. and with their hydrophobicities. Given the exptl. conditions, and the amino acid composition, it is possible to calculate the retention time of a peptide eluted by a gradient, for any slope of gradient, flow-rate, and column length.
IT **116685-54-2**
RL: ANT (Analyte); ANST (Analytical study)
(chromatog. of, reversed-phase high-performance liquid, retention time of, prediction of)

L2 ANSWER 23 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 01 Nov 1985
ACCESSION NUMBER: 1985:539885 HCAPLUS
DOCUMENT NUMBER: 103:139885
TITLE: T cell recognition of myoglobin. Localization of the sites stimulating T cell proliferative responses by synthetic overlapping peptides encompassing the entire molecule
AUTHOR(S): Bixler, Garvin S., Jr.; Atassi, M. Zouhair
CORPORATE SOURCE: Verna and Marrs McLean Dep. Biochem., Baylor Coll. Med., Houston, TX, 77030, USA

SOURCE: Journal of Immunogenetics (1984), 11(5-6), 339-53
CODEN: JIMGAV; ISSN: 0305-1811
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A comprehensive strategy for the systematic localization of all continuous antigenic sites within a protein was previously introduced. The strategy consists of studying the immunochem. activity of a series of consecutive synthetic peptides that encompass the entire protein chain and that are uniform in size and in overlap at their N- and C-terminals with neighboring peptides. By application of this strategy to sperm whale myoglobin, the authors were able to delineate the continuous sites of T cell recognition of myoglobin in 3 high responder mouse strains. Thirteen 17-residue peptides that encompass the entire myoglobin chain and overlap by 5 residues at both ends were synthesized, purified and characterized. The peptides were examined in vitro for their ability to stimulate lymph node cells from myoglobin-primed DBA/2 (H-2d), BALB/c (H-2d) and SJL (H-2s) mice as well as long-term cultures of myoglobin-specific T cells. Several regions of the mol. (T sites) stimulated myoglobin-primed lymph node cells and myoglobin-specific longterm T cell cultures. This strategy has enabled the localization of the full profile of dominant sites of T cell recognition in myoglobin for these mouse strains. Of these T sites, one region, residues 107-125, was clearly immunodominant in these strains and coincided with the antigenic (i.e. antibody binding) site 4 of myoglobin. Also, other regions stimulated T cells and appeared to coincide with previously known antigenic sites. It is noteworthy that, in addition to sites recognized by both T and B cells, the myoglobin protein has other sites which are recognized exclusively by T cells and to which no detectable antibody response is directed.

IT **88530-81-8**
RL: PROC (Process)
(T-lymphocyte recognition of, of myoglobin)

IT **98474-13-6P**
RL: PREP (Preparation)
(preparation and T-lymphocyte recognition of, of myoglobin)

L2 ANSWER 24 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 12 May 1984
ACCESSION NUMBER: 1984:49896 HCAPLUS
DOCUMENT NUMBER: 100:49896
TITLE: Preparation of T-lymphocyte lines and clones with specificities to preselected protein sites by in vitro passage with free synthetic peptides: demonstration with myoglobin sites
AUTHOR(S): Yoshioka, Mitsuaki; Bixler, Garvin S., Jr.; Atassi, M. Zouhair
CORPORATE SOURCE: Dep. Immunol., Mayo Clin., Rochester, MN, 55905, USA
SOURCE: Molecular Immunology (1983), 20(10), 1133-7
CODEN: MOIMD5; ISSN: 0161-5890
DOCUMENT TYPE: Journal
LANGUAGE: English

AB It was previously demonstrated that antibodies to preselected

regions of a protein can be obtained by immunization with free small synthetic peptides (6-7 residues) without conjugation to a carrier. Here, the use of free synthetic peptides representing myoglobin (Mb) antigenic sites to prepare T-cell lines and clones of preselected specificities is reported. Lymph node cells from mice primed in vivo with sperm whale Mb were periodically passaged in vitro with synthetic peptide. After several passages, the peptide-driven long term T-cell cultures responded to the intact protein and exclusively to the peptide that was used to drive the cells. From these cultures, T-cell clones were prepared that responded only to the driving peptide and to the whole protein. The ability to prepare T-cell lines and T-cell clones with preselected submol. specificities to a protein by driving cultures with desired synthetic peptides affords an important and simple tool for basic immunol. investigations and for clin. applications.

IT **88530-81-8P**
RL: PREP (Preparation)
(preparation of and T-lymphocyte cell lines and clones specific for, as myoglobin peptide analogs)

L2 ANSWER 25 OF 25 HCAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 12 May 1984
ACCESSION NUMBER: 1979:87867 HCAPLUS
DOCUMENT NUMBER: 90:87867
TITLE: Synthesis of protected sequences 81-88, 89-94, 83-94 and 81-94 of the F-region of myoglobin
AUTHOR(S): Eckstein, Heiner; Bayer, Ernst
CORPORATE SOURCE: Inst. Org. Chem., Univ. Tuebingen, Tuebingen, Fed. Rep. Ger.
SOURCE: Justus Liebigs Annalen der Chemie (1978), (10), 1607-16
CODEN: JLACBF; ISSN: 0075-4617
DOCUMENT TYPE: Journal
LANGUAGE: German
AB The myoglobin 89-94 sequence, H-Leu-Ala-Gln-Ser(CMe3)-His-Ala-OMe (I), was prepared by coupling Z-Leu-Ala-OH (Z = PhCH2O2C) to H-Gln-Ser(CMe3)-His-Ala-OMe by the mixed anhydride method and Z-deblocking the resulting hexapeptide, whereas the protected 83-88 myoglobin sequence, Z-Glu(OCMe3)-Ala-Glu(OCMe3)-Leu-Lys(BOC)-Pro-NHNH2 (II, BOC = CO2CMe3), was prepared by coupling Z-Glu(OCMe3)-Ala-Glu(OCMe3)-NHNH2 to H-Leu-Lys(BOC)-Pro-OMe by the azide method and treating the resulting hexapeptide Me ester with NH2NH2. I was coupled to II by the azide method to give the Z-protected 80-94 sequence which was Z-deblocked to give H-Glu(OCMe3)-Ala-Glu(OCMe3)-Leu-Lys(BOC)-Pro-Leu-Ala-Glu-Ser(CMe3)-His-Ala-OMe (III). The attempted coupling of Z-His-His-NHNH2 (IV) (myoglobin sequence 81-82) with III by the azide method to give the 81-94 sequence (V) was not successful. The 81-88 sequence, Z-His-His-Glu(OCMe3)-Ala-Glu(OCMe3)-Leu-Lys(BOC)-Pro-NHNH2 (VI), was prepared by coupling IV to H-Glu(OCMe3)-Ala-Glu(OCMe3)-Leu-Lys(BOC)-Pro-OMe and treating the resulting peptide Me ester with NH2NH2. The attempted azide coupling of VI with I to give V also failed.

IT **69323-25-7P**
RL: SPN (Synthetic preparation); PREP (Preparation)
(attempted preparation of, failure of attempted azide fragment condensation in relation to)

IT **69323-24-6P**
RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation); RACT (Reactant or reagent)
(preparation and attempted peptide coupling of, with dipeptide azide)
IT **69323-19-9P**
RL: SPN (Synthetic preparation); PREP (Preparation)
(preparation and partial deblocking of)

E1 THROUGH E29 ASSIGNED

FILE 'REGISTRY' ENTERED AT 09:59:15 ON 05 APR 2004
L3 29 SEA FILE=REGISTRY ABB=ON PLU=ON (126301-55-1/BI OR 88530-81-8/BI OR 118024-72-9/BI OR 126301-54-0/BI OR 214628-28-1/BI OR 478412-67-8/BI OR 478412-68-9/BI OR 116685-54-2/BI OR 142473-27-6/BI OR 142473-29-8/BI OR 142473-35-6/BI OR 144505-38-4/BI OR 149183-28-8/BI OR 189134-95-0/BI OR 398148-67-9/BI OR 398148-70-4/BI OR 422320-93-2/BI OR 437767-29-8/BI OR 495402-07-8/BI OR 503535-18-0/BI OR 518998-85-1/BI OR 557064-43-4/BI OR 557064-44-5/BI OR 557064-45-6/BI OR 574743-62-7/BI OR 69323-19-9/BI OR 69323-24-6/BI OR 69323-25-7/BI OR 98474-13-6/BI)

L4 29 L1 AND L3

L4 ANSWER 1 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **574743-62-7** REGISTRY
CN L-Tryptophan, L-prolyl-L-alanyl-L-alanyl-L-leucyl-L-histidyl-L-histidyl-L-alanyl-L-leucyl-L-alanyl-L-leucyl-L-alanyl-L-histidyl-L-histidyl-L-leucyl- (9CI) (CA INDEX NAME)
SQL **15**

SEQ 1 PAALHHALAL AHHLW
=======
HITS AT: 1-7

REFERENCE 1: 139:163463

L4 ANSWER 2 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **557064-45-6** REGISTRY
CN L-Lysine, glycyl-L-histidyl-L-histidyl-L-α-glutamyl-L-alanyl-L-α-glutamyl-L-leucyl-L-lysyl-L-prolyl-L-leucyl-L-alanyl-L-glutaminyl-L-seryl-L-histidyl-L-alanyl-L-threonyl- (9CI) (CA INDEX NAME)
SQL **17**

SEQ 1 GHHEAELKPL AQSHATK
== =====
HITS AT: 9-15

REFERENCE 1: 139:97654

L4 ANSWER 3 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **557064-44-5** REGISTRY
CN L-Lysine, L-lysylglycyl-L-histidyl-L-histidyl-L-α-glutamyl-L-alanyl-L-α-glutamyl-L-leucyl-L-lysyl-L-prolyl-L-leucyl-L-

alanyl-L-glutaminyl-L-seryl-L-histidyl-L-alanyl-L-threonyl- (9CI)
(CA INDEX NAME)
SQL **18**

SEQ 1 KGHHEAELKP LAQSHATK
= ======

HITS AT: 10-16

REFERENCE 1: 139:97654

L4 ANSWER 4 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **557064-43-4** REGISTRY
CN L-Lysine, L-lysyl-L-lysylglycyl-L-histidyl-L-histidyl-L-α-glutamyl-L-alanyl-L-α-glutamyl-L-leucyl-L-lysyl-L-prolyl-L-leucyl-L-alanyl-L-glutaminyl-L-seryl-L-histidyl-L-alanyl-L-threonyl- (9CI) (CA INDEX NAME)
SQL **19**

SEQ 1 KKGHHEAELK PLAQSHATK
=======

HITS AT: 11-17

REFERENCE 1: 139:97654

L4 ANSWER 5 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **518998-85-1** REGISTRY
CN L-Tyrosine, L-seryl-L-phenylalanyl-L-lysyl-L-prolyl-L-prolyl-L-alanyl-L-asparaginyl-L-histidyl-L-histidyl-L-alanyl-L-tryptophyl- (9CI) (CA INDEX NAME)
SQL **12**

SEQ 1 SFKPPANHHA WY
=======

HITS AT: 4-10

REFERENCE 1: 138:348758

L4 ANSWER 6 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **503535-18-0** REGISTRY
CN L-Arginine, L-alanylglycyl-L-α-glutamyl-L-prolyl-L-histidyl-L-alanyl-L-α-glutamyl-L-valyl-L-histidyl-L-alanyl-L-leucyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 82: PN: WO03025006 FIGURE: 8 unclaimed sequence
SQL **12**

SEQ 1 AGEPHAEVHA LR
=======

HITS AT: 4-10

REFERENCE 1: 138:267686

L4 ANSWER 7 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **495402-07-8** REGISTRY
CN L-Alanine, L-valyl-L-valyl-L-seryl-L-valyl-L-valyl-L-prolylglycyl-L-alanyl-L-isoleucyl-L-seryl-L-histidyl- (9CI) (CA INDEX NAME)

SQL **12**

SEQ 1 VVSVVPGAIS HA
===== ==

HITS AT: 6-12

REFERENCE 1: 138:150397

L4 ANSWER 8 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **478412-68-9** REGISTRY
CN L-Alanine, L-prolyl-3-cyclohexyl-L-alanyl-L-alanylglycyl-S-methyl-L-cysteinyl-L-histidyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 15: PN: US20020193298 SEQID: 17 claimed protein
SQL **7**

SEQ 1 PAAGCHA
=======

HITS AT: 1-7

REFERENCE 1: 139:7179

REFERENCE 2: 138:33374

L4 ANSWER 9 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **478412-67-8** REGISTRY
CN L-Alanine, L-prolyl-3-cyclohexyl-L-alanyl-L-alanyl-(2S)-2-aminobutanoyl-S-methyl-L-cysteinyl-L-histidyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 14: PN: US20020193298 SEQID: 16 claimed protein
SQL **7**

SEQ 1 PAAXCHA
=======

HITS AT: 1-7

REFERENCE 1: 139:7179

REFERENCE 2: 138:33374

L4 ANSWER 10 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **437767-29-8** REGISTRY
CN L-Alanine, L-histidyl-L-leucyl-L-phenylalanyl-L-seryl-L-seryl-L-prolyl-L-arginyl-L-alanyl-L-isoleucyl-L-α-glutamyl-L-histidyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 8: PN: WO0248349 SEQID: 9 unclaimed sequence
SQL **12**

SEQ 1 HLFSSPRAIE HA
===== ==

HITS AT: 6-12

REFERENCE 1: 137:43263

L4 ANSWER 11 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **422320-93-2** REGISTRY
CN L-Leucine, L-leucyl-L-leucyl-L-glutaminyl-L-prolyl-L-prolyl-L-alanyl-L-arginylglycyl-L-histidyl-L-alanyl-L-histidyl-L-α-aspartylglycyl-L-glutaminyl-L-alanyl-L-leucyl-L-seryl-L-threonyl-L-α-aspartyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 22: PN: WO0236771 PAGE: 183 claimed protein
SQL **20**

SEQ 1 LLQPPARGHA HDGQALSTDL
=======
HITS AT: 4-10

REFERENCE 1: 136:364964

L4 ANSWER 12 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **398148-70-4** REGISTRY
CN Rhodium(1+), [μ-[N-[4-(4'-methyl[2,2'-bipyridin]-4-yl-κN1,κN1')-1-oxobutyl]-L-α-aspartyl-L-prolyl-L-α-aspartyl-L-alanyl-L-leucyl-L-α-glutamyl-L-histidyl-κN1-L-alanyl-L-alanyl-L-lysyl-L-histidyl-κN1-L-α-glutamyl-L-alanyl-L-alanyl-L-alanyl-L-lysinamidato(4-)]]bis[9,10-phenanthrenediaminato(2-)-κN,κN'](zinc)-, conjugate tetraacid (9CI) (CA INDEX NAME)
CI CCS
SQL **16**

SEQ 1 DPDALEHAAK HEAAAK
=======
HITS AT: 2-8

REFERENCE 1: 136:163197

L4 ANSWER 13 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **398148-67-9** REGISTRY
CN Rhodium, [μ-[N-[4-(4'-methyl[2,2'-bipyridin]-4-yl-κN1,κN1')-1-oxobutyl]-L-α-aspartyl-L-prolyl-L-α-aspartyl-L-alanyl-L-leucyl-L-α-glutamyl-L-histidyl-κN1-L-alanyl-L-alanyl-L-lysyl-L-histidyl-κN1-L-α-glutamyl-L-alanyl-L-α-glutamyl-L-alanyl-L-lysinamidato(5-)]]bis[9,10-phenanthrenediaminato(2-)-κN,κN'](zinc)-, conjugate pentaacid (9CI) (CA INDEX NAME)
CI CCS
SQL **16**

SEQ 1 DPDALEHAAK HEAEAK
=======
HITS AT: 2-8

REFERENCE 1: 136:163197

L4 ANSWER 14 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **214628-28-1** REGISTRY
CN Glycine, L-prolyl-L-α-aspartyl-L-alanyl-L-α-aspartyl-L-alanyl-L-histidyl-L-alanyl-L-histidyl-L-alanyl-L-histidyl-L-alanyl-L-

alanyl-L-alanyl-L-histidyl- (9CI) (CA INDEX NAME)
SQL **15**

SEQ 1 PDADAHAHAH AAAHG
=======
HITS AT: 1-7

REFERENCE 1: 137:321810

REFERENCE 2: 129:302879

L4 ANSWER 15 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **189134-95-0** REGISTRY
CN L-Alaninamide, N-acetyl-L-α-glutamyl-L-leucyl-L-lysyl-L-prolyl-L-leucyl-L-alanyl-L-glutaminyl-L-seryl-L-histidyl- (9CI) (CA INDEX NAME)
SQL **10**

SEQ 1 ELKPLAQSHA
=======
HITS AT: 4-10

REFERENCE 1: 126:302757

L4 ANSWER 16 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **149183-28-8** REGISTRY
CN L-Aspartic acid, L-α-glutamylglycylglycyl-L-α-glutamyl-L-prolyl-L-cysteinyl-L-alanyl-L-cysteinyl-L-prolyl-L-histidyl-L-alanyl-L-leucyl-L-histidyl-L-arginyl-L-valyl-L-cysteinylglycyl-L-seryl- (9CI) (CA INDEX NAME)
SQL **19**

SEQ 1 EGGEPCACPH ALHRVCGSD
====== =
HITS AT: 5-11

REFERENCE 1: 119:90109

L4 ANSWER 17 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **144505-38-4** REGISTRY
CN L-Alanine, N-[N-[N-[N-[N-[N-[N-[N-[1-(N-L-methionyl-L-alanyl)-L-prolyl]-L-histidyl]-L-alanyl]-L-histidyl]-L-alanyl]-L-histidyl]-L-alanyl]-L-histidyl]- (9CI) (CA INDEX NAME)
SQL **11**

SEQ 1 MAPHAHAHAH A
=======
HITS AT: 3-9

REFERENCE 1: 118:11732

L4 ANSWER 18 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **142473-35-6** REGISTRY
CN L-Lysine, N2-[N-[N-[N-[N-[N2-[N-[N-[1-[N2-[N-(5-oxo-L-prolyl)-L-leucyl]-L-lysyl]-L-prolyl]-L-leucyl]-L-alanyl]-L-glutaminyl]-L-seryl]-L-histidyl]-L-alanyl]-L-threonyl]-, trifluoroacetate (salt)

(9CI) (CA INDEX NAME)
SQL **12**

SEQ 1 XLKPLAQSHA TK
=======
HITS AT: 4-10

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 117:70320

L4 ANSWER 19 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **142473-29-8** REGISTRY
CN L-Lysine, L-lysyl-L-lysyl-L-lysylglycyl-L-histidyl-L-histidyl-L-α-glutamyl-L-alanyl-L-α-glutamyl-L-leucyl-L-lysyl-L-prolyl-L-leucyl-L-alanyl-L-glutaminyl-L-seryl-L-histidyl-L-alanyl-L-threonyl-, hexaacetate (salt) (9CI) (CA INDEX NAME)
SQL **20**

SEQ 1 KKKGHHEAEL KPLAQSHATK
=======
HITS AT: 12-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 117:70320

L4 ANSWER 20 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **142473-27-6** REGISTRY
CN L-Lysine, N2-[N-[N-[N-[N-[N2-[N-[N-[1-[N2-(N-L-α-glutamyl-L-leucyl)-L-lysyl]-L-prolyl]-L-leucyl]-L-alanyl]-L-glutaminyl]-L-seryl]-L-histidyl]-L-alanyl]-L-threonyl]-, octakis(trifluoroacetate) (salt) (9CI) (CA INDEX NAME)
SQL **12**

SEQ 1 ELKPLAQSHA TK
=======
HITS AT: 4-10

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 117:70320

L4 ANSWER 21 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **126301-55-1** REGISTRY
CN L-Lysine, N2-[(1,1-dimethylethoxy)carbonyl]-N6-[(phenylmethoxy)carbonyl]-L-lysyl-N6-[(phenylmethoxy)carbonyl]-L-lysyl-N6-[(phenylmethoxy)carbonyl]-L-lysylglycyl-L-histidyl-L-histidyl-L-α-glutamyl-L-alanyl-L-α-glutamyl-L-leucyl-N6-[(phenylmethoxy)carbonyl]-L-lysyl-L-prolyl-L-leucyl-L-alanyl-L-glutaminyl-O-(phenylmethyl)-L-seryl-L-histidyl-L-alanyl-L-threonyl-N6-[(phenylmethoxy)carbonyl]-, tris(phenylmethyl) ester (9CI) (CA INDEX NAME)
SQL **20**

SEQ 1 KKKGHHEAEL KPLAQSHATK

=======

HITS AT: 12-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 118:255311

REFERENCE 2: 117:70320

REFERENCE 3: 112:179814

L4 ANSWER 22 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **126301-54-0** REGISTRY
CN L-Lysine, N2-[N-[N-[N-[N-[N2-[N-[N-[1-[N2-[N-[N-[(1,1-dimethylethoxy)carbonyl]-L-α-glutamyl]-L-leucyl]-N6-[(phenylmethoxy)carbonyl]-L-lysyl]-L-prolyl]-L-leucyl]-L-alanyl]-L-glutaminyl]-O-(phenylmethyl)-L-seryl]-L-histidyl]-L-alanyl]-L-threonyl]-N6-[(phenylmethoxy)carbonyl]-, bis(phenylmethyl) ester (9CI) (CA INDEX NAME)
SQL **12**

SEQ 1 ELKPLAQSHA TK
=======

HITS AT: 4-10

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 117:70320

REFERENCE 2: 112:179814

L4 ANSWER 23 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **118024-72-9** REGISTRY
CN L-Proline, L-lysyl-L-prolyl-L-leucyl-L-alanyl-L-glutaminyl-L-seryl-L-histidyl-L-alanyl-L-threonyl-L-lysyl-L-histidyl-L-lysyl-L-isoleucyl- (9CI) (CA INDEX NAME)
SQL **14**

SEQ 1 KPLAQSHATK HKIP
=======

HITS AT: 2-8

REFERENCE 1: 127:204167

REFERENCE 2: 110:21983

L4 ANSWER 24 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **116685-54-2** REGISTRY
CN L-Lysine, glycyl-L-histidyl-L-histidyl-L-α-glutamyl-L-alanyl-L-α-glutamyl-L-leucyl-L-lysyl-L-prolyl-L-leucyl-L-alanyl-L-α-glutamyl-L-seryl-L-histidyl-L-alanyl-L-threonyl- (9CI) (CA INDEX NAME)
SQL **17**

SEQ 1 GHHEAELKPL AESHATK
== =====

HITS AT: 9-15

REFERENCE 1: 109:145522

L4 ANSWER 25 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **98474-13-6** REGISTRY
CN L-Isoleucine, L-α-glutamyl-L-leucyl-L-lysyl-L-prolyl-L-leucyl-L-alanyl-L-glutaminyl-L-seryl-L-histidyl-L-alanyl-L-threonyl-L-lysyl-L-histidyl-L-lysyl-L-isoleucyl-L-prolyl- (9CI) (CA INDEX NAME)
SQL **17**

SEQ 1 ELKPLAQSHA TKHKIPI
=======
HITS AT: 4-10

REFERENCE 1: 103:139885

L4 ANSWER 26 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **88530-81-8** REGISTRY
CN L-Proline, L-lysyl-L-prolyl-L-leucyl-L-alanyl-L-α-glutamyl-L-seryl-L-histidyl-L-alanyl-L-threonyl-L-lysyl-L-histidyl-L-lysyl-L-isoleucyl- (9CI) (CA INDEX NAME)
SQL **14**

SEQ 1 KPLAESHATK HKIP
=======
HITS AT: 2-8

REFERENCE 1: 112:116832

REFERENCE 2: 103:139885

REFERENCE 3: 100:49896

L4 ANSWER 27 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **69323-25-7** REGISTRY
CN L-Alanine, N-[(phenylmethoxy)carbonyl]-L-histidyl-L-histidyl-L-α-glutamyl-L-alanyl-L-α-glutamyl-L-leucyl-N6-[(1,1-dimethylethoxy)carbonyl]-L-lysyl-L-prolyl-L-leucyl-L-alanyl-L-glutaminyl-O-(1,1-dimethylethyl)-L-seryl-L-histidyl-, 3,5-bis(1,1-dimethylethyl) 14-methyl ester (9CI) (CA INDEX NAME)
SQL **14**

SEQ 1 HHEAELKPLA QSHA
=== ====
HITS AT: 8-14

REFERENCE 1: 90:87867

L4 ANSWER 28 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **69323-24-6** REGISTRY
CN L-Alanine, N-[N-[N-[N2-[N-[N-[1-[N6-[(1,1-dimethylethoxy)carbonyl]-N2-[N-[N-(N-L-α-glutamyl-L-alanyl)-L-α-glutamyl]-L-leucyl]-L-lysyl]-L-prolyl]-L-leucyl]-L-alanyl]-L-glutaminyl]-O-(1,1-dimethylethyl)-L-seryl]-L-histidyl]-, 5,5'-bis(1,1-dimethylethyl) 1-methyl ester (9CI) (CA INDEX NAME)

SQL **12**

SEQ 1 EAELKPLAQS HA
=====
HITS AT: 6-12

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 90:87867

L4 ANSWER 29 OF 29 REGISTRY COPYRIGHT 2004 ACS on STN
RN **69323-19-9** REGISTRY
CN L-Alanine, N-[N-[N-[N2-[N-[N-[1-[N2-[N-[N-[N-[N-[(phenylmethoxy)carbonyl]-L-α-glutamyl]-L-alanyl]-L-α-glutamyl]-L-leucyl]-L-lysyl]-L-prolyl]-L-leucyl]-L-alanyl]-L-glutaminyl]-O-(1,1-dimethylethyl)-L-seryl]-L-histidyl]-, 5,5'-bis(1,1-dimethylethyl) 1-methyl ester (9CI) (CA INDEX NAME)
SQL **12**

SEQ 1 EAELKPLAQS HA
=====
HITS AT: 6-12

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 90:87867

FILE 'HOME' ENTERED AT 09:59:42 ON 05 APR 2004

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 5, 2004, 09:01:27 ; Search time 39 Seconds
(without alignments)
56.631 Million cell updates/sec

Title: US-09-972-772A-16
Perfect score: 26
Sequence: 1 PXAXXHA 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 7668

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	17	65.4	10	11	Q91WZ3	Q91wz3 rattus sp.
2	17	65.4	14	4	Q93057	Q93057 homo sapien
3	17	65.4	14	11	P70319	P70319 mus musculu
4	16	61.5	15	2	Q9R541	Q9r541 mycobacteri
5	16	61.5	15	5	Q9TWT4	Q9twt4 lumbricus t
6	16	61.5	19	12	O90628	O90628 simian herp
7	16	61.5	19	12	O90622	O90622 simian herp
8	16	61.5	19	12	O90635	O90635 simian herp
9	15	57.7	20	10	Q9S934	Q9s934 petunia hyb
10	14	53.8	10	4	Q8NER0	Q8ner0 homo sapien
11	14	53.8	15	6	Q9TRL0	Q9trl0 canis famil
12	14	53.8	16	10	Q8W1B4	Q8w1b4 oryza sativ
13	14	53.8	16	11	Q9QZY3	Q9qzy3 mus musculu
14	14	53.8	20	4	O95108	O95108 homo sapien
15	13	50.0	14	2	P71199	P71199 escherichia
16	13	50.0	14	2	O85527	O85527 chlamydia t
17	13	50.0	15	6	Q9TRL3	Q9trl3 ovis aries
18	13	50.0	15	8	Q95771	Q95771 ctenosaura
19	13	50.0	15	8	Q95952	Q95952 sauromalus
20	13	50.0	15	8	Q95879	Q95879 phrynosoma
21	13	50.0	15	8	Q37016	Q37016 nicotiana a
22	13	50.0	16	6	Q8WMZ0	Q8wmz0 canis famil
23	13	50.0	16	8	Q9T2I6	Q9t2i6 nicotiana s
24	13	50.0	16	8	Q36789	Q36789 solanum nig
25	13	50.0	19	8	Q36925	Q36925 nicotiana v
26	13	50.0	19	15	Q90RE9	Q90re9 human immun
27	13	50.0	19	15	Q905I4	Q905i4 human immun
28	13	50.0	20	4	O75318	O75318 homo sapien
29	13	50.0	20	5	Q9TWR0	Q9twr0 blattella g
30	13	50.0	20	8	Q9T2I9	Q9t2i9 nicotiana s
31	13	50.0	20	8	Q36584	Q36584 nicotiana g
32	13	50.0	20	8	Q9T2I8	Q9t2i8 nicotiana s
33	13	50.0	20	13	Q9PSI5	Q9psi5 oncorhynchu
34	13	50.0	20	13	Q9PSI4	Q9psi4 oncorhynchu
35	12	46.2	7	2	P72081	P72081 nocardia la
36	12	46.2	8	5	Q8MUN6	Q8mun6 heliconius
37	12	46.2	8	5	Q86BS9	Q86bs9 strongyloce
38	12	46.2	9	2	Q47410	Q47410 escherichia
39	12	46.2	9	4	Q14277	Q14277 homo sapien
40	12	46.2	9	8	P92072	P92072 euhadra her
41	12	46.2	10	5	Q8MUP1	Q8mup1 heliconius
42	12	46.2	10	5	Q8MUN7	Q8mun7 heliconius
43	12	46.2	10	5	P82223	P82223 bombyx mori
44	12	46.2	10	5	P82224	P82224 bombyx mori
45	12	46.2	10	6	Q9TS42	Q9ts42 sus scrofa
46	12	46.2	11	2	Q8KHL0	Q8khl0 streptococc
47	12	46.2	11	2	Q8KRA1	Q8kra1 streptococc
48	12	46.2	11	5	Q8MM58	Q8mm58 heliconius
49	12	46.2	11	6	Q9BDC8	Q9bdc8 pongo pygma
50	12	46.2	11	6	Q9XSP7	Q9xsp7 pygathrix n
51	12	46.2	11	6	Q9XSP2	Q9xsp2 hylobates s
52	12	46.2	11	6	Q9BDQ9	Q9bdq9 gorilla gor
53	12	46.2	11	6	Q9XSP5	Q9xsp5 pan troglod
54	12	46.2	11	6	Q9BDD0	Q9bdd0 pan troglod
55	12	46.2	11	6	Q9XSP8	Q9xsp8 presbytis j
56	12	46.2	11	6	Q9XSP6	Q9xsp6 pongo pygma
57	12	46.2	11	6	Q9BDC9	Q9bdc9 pan paniscu

58 12 46.2 11 6 Q9XSQ4 Q9xsq4 gorilla gor

ALIGNMENTS

RESULT 1
Q91WZ3
ID Q91WZ3 PRELIMINARY; PRT; 10 AA.
AC Q91WZ3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Luteinizing hormone/chorionic gonadotropin receptor homolog
DE (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=96147985; PubMed=8571710;
RA Shen Q.X., Liu H.H., Chen W.Y., Bahl O.P.;
RT "[Cloning and overexpression of rat ovary LH/hCG receptor cDNA in
RT insect cells].";
RL Shih Yen Sheng Wu Hsueh Pao 28:283-290(1995).
DR EMBL; S80660; AAB50710.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005213; F:structural constituent of chorion (sensu In. . .; IEA.
KW Chorion; Receptor.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1129 MW; 09A5F22DC4177760 CRC64;

Query Match 65.4%; Score 17; DB 11; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 PXAXXH 6
              | |  |
Db          5 PRALTH 10
```

Search completed: April 5, 2004, 09:05:22
Job time : 62 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 5, 2004, 08:58:12 ; Search time 11 Seconds
(without alignments)
33.136 Million cell updates/sec

Title: US-09-972-772A-16
Perfect score: 26
Sequence: 1 PXAXXHA 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 1238

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16	61.5	20	1	RT16_BOVIN	P82915 bos taurus
2	14	53.8	20	1	DER6_DERPT	P49277 dermatophag
3	14	53.8	20	1	HGL1_FASHE	P80527 fasciola he
4	14	53.8	20	1	PL5_LUPLU	P83367 lupinus lut
5	13	50.0	13	1	BLAC_STRGR	P81173 streptomyce
6	13	50.0	13	1	CXA2_CONGE	P01520 conus geogr
7	13	50.0	15	1	CXA1_CONGE	P01519 conus geogr
8	13	50.0	19	1	COXR_THUOB	P80984 thunnus obe
9	13	50.0	20	1	RECX_AZOVI	P37863 azotobacter
10	12	46.2	8	1	LCK4_LEUMA	P21143 leucophaea
11	12	46.2	9	1	XYLA_STRSQ	P19149 streptomyce
12	12	46.2	10	1	COXA_ONCMY	P80328 oncorhynchu
13	12	46.2	10	1	GON2_CHEPR	P80678 chelyosoma
14	12	46.2	10	1	TKL4_LOCMI	P30250 locusta mig
15	12	46.2	10	1	TRP8_LEUMA	P81740 leucophaea
16	12	46.2	12	1	RS19_CLYEP	Q46490 clover yell
17	12	46.2	12	1	RS19_ELYEP	Q47881 elm yellows

18	12	46.2	14	1	ADFA_TENMO	P82965 tenebrio mo
19	12	46.2	14	1	BGAT_MOUSE	P38649 m histo-blo
20	12	46.2	14	1	RS19_CLOPP	Q46228 clover prol
21	12	46.2	14	1	RS19_LOWBP	Q48878 loofah witc
22	12	46.2	15	1	SODP_PINPS	P81082 pinus pinas
23	12	46.2	19	1	PTHP_STRSA	P24365 streptococc
24	12	46.2	20	1	ALAT_PIG	P13191 sus scrofa
25	12	46.2	20	1	ATP4_SPIOL	P80085 spinacia ol
26	12	46.2	20	1	CRP_MUSCA	P19094 mustelus ca
27	12	46.2	20	1	ELAS_GADMO	P32197 gadus morhu
28	12	46.2	20	1	FRE3_LITIN	P56249 litoria inf
29	12	46.2	20	1	LPP2_HUMAN	P56642 homo sapien
30	11	42.3	9	1	LITR_PHYRO	P08946 phyllomedus
31	11	42.3	9	1	TKC1_CALVO	P41517 calliphora
32	11	42.3	10	1	TRP6_LEUMA	P81738 leucophaea
33	11	42.3	11	1	LPW_THETH	P05624 thermus the
34	11	42.3	11	1	RANC_RANPI	P08951 rana pipien
35	11	42.3	12	1	LMT1_LOCMI	P22395 locusta mig
36	11	42.3	12	1	TA10_TREME	P01371 tremella me
37	11	42.3	13	1	PSAE_PEA	P20118 pisum sativ
38	11	42.3	14	1	UHA1_CANFA	P99503 canis famil
39	11	42.3	15	1	GTS_ASADI	P83246 asaphis dic
40	11	42.3	15	1	UC08_MAIZE	P80614 zea mays (m
41	11	42.3	15	1	UN01_PINPS	P81106 pinus pinas
42	11	42.3	16	1	SAL3_ONCMY	P82240 oncorhynchu
43	11	42.3	16	1	SSIT_STRMB	P83544 streptomyce
44	11	42.3	17	1	A45K_MYCBO	P80069 mycobacteri
45	11	42.3	17	1	BOL5_MEGPE	P07496 megabombus
46	11	42.3	17	1	BTID_BOOMI	P83607 boophilus m
47	11	42.3	17	1	RANR_RANRU	P08952 rana rugosa
48	11	42.3	17	1	YALA_TRYBB	P17961 trypanosoma
49	11	42.3	18	1	HEX_ADECU	P35985 canine aden
50	11	42.3	18	1	MLB_HORSE	P01202 equus cabal
51	11	42.3	19	1	ANP7_ELEGR	P11920 eleginus gr
52	11	42.3	19	1	PHSL_DESBN	P13066 desulfovibr
53	11	42.3	19	1	PSAE_CUCSA	P42047 cucumis sat
54	11	42.3	20	1	ABP_PIG	Q9trc7 sus scrofa
55	11	42.3	20	1	COG1_CHIOP	P34153 chionoecete
56	11	42.3	20	1	MCRG_METTE	P22950 methanosarc
57	10	38.5	7	1	ALL3_CARMA	P81806 carcinus ma
58	10	38.5	7	1	ALL4_CARMA	P81807 carcinus ma
59	10	38.5	7	1	ALL5_CARMA	P81808 carcinus ma
60	10	38.5	7	1	MNP1_LEPDE	P42984 leptinotars
61	10	38.5	8	1	ALL7_CARMA	P81809 carcinus ma
62	10	38.5	8	1	ALL8_CARMA	P81811 carcinus ma
63	10	38.5	8	1	ALL9_CARMA	P81812 carcinus ma
64	10	38.5	8	1	CLP_THICU	P80488 thiobacillu
65	10	38.5	8	1	PPK2_PERAM	P82692 periplaneta
66	10	38.5	9	1	AL10_CARMA	P81813 carcinus ma
67	10	38.5	9	1	LITO_LITAU	P08945 litoria aur
68	10	38.5	9	1	NEUX_HUMAN	P04277 homo sapien
69	10	38.5	9	1	RT33_BOVIN	P82926 bos taurus
70	10	38.5	10	1	FARP_MYTED	P42560 mytilus edu
71	10	38.5	10	1	GRP_RANRI	P23260 rana ridibu
72	10	38.5	10	1	TKL3_LOCMI	P30249 locusta mig
73	10	38.5	10	1	UXB1_YEAST	P99012 saccharomyc
74	10	38.5	11	1	TKN1_UPEIN	P82026 uperoleia i

ALIGNMENTS

```
RESULT 1
RT16_BOVIN
ID   RT16_BOVIN     STANDARD;      PRT;    20 AA.
AC   P82915;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Mitochondrial 28S ribosomal protein S16 (MRP-S16) (Fragments).
GN   MRPS16 OR RPMS16.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Liver;
RX   MEDLINE=21276436; PubMed=11279123;
RA   Koc E.C., Burkhart W., Blackburn K., Moseley A., Spremulli L.L.;
RT   "The small subunit of the mammalian mitochondrial ribosome:
RT   identification of the full complement of ribosomal proteins present.";
RL   J. Biol. Chem. 276:19363-19374(2001).
CC   -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC       (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC   -!- SUBCELLULAR LOCATION: Mitochondrial.
CC   -!- SIMILARITY: Belongs to the S16P family of ribosomal proteins.
DR   InterPro; IPR000307; Ribosomal_S16.
DR   PROSITE; PS00732; RIBOSOMAL_S16; PARTIAL.
KW   Ribosomal protein; Mitochondrion.
FT   NON_TER       1      1
FT   NON_CONS      9     10
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2205 MW;  BC042AC57F236CE5 CRC64;

  Query Match             61.5%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   42.9%;  Pred. No. 2e+02;
  Matches    3;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 PXAXXHA 7
              |    ||
Db          1 PMPNSHA 7


Search completed: April  5, 2004, 09:04:23
Job time : 27 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 5, 2004, 09:01:52 ; Search time 20 Seconds
(without alignments)
33.667 Million cell updates/sec

Title: US-09-972-772A-16
Perfect score: 26
Sequence: 1 PXAXXHA 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 3885

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	65.4	12	2	S65730	hemoglobin, extrac
2	16	61.5	15	2	S36893	ribosomal protein
3	16	61.5	20	2	S72501	protein kinase C i
4	15	57.7	20	2	PH0110	style glycoprotein
5	14	53.8	14	2	PL0142	carbon-monoxide de
6	14	53.8	15	2	B45133	casein kinase II (
7	14	53.8	20	2	S15861	estrogen receptor
8	13	50.0	5	2	JN0860	peptidyl-dipeptida
9	13	50.0	13	1	NTKN2G	alpha-conotoxin GI
10	13	50.0	14	2	S22236	lipoxygenase (EC 1
11	13	50.0	15	1	NTKNAG	alpha-conotoxin GI
12	13	50.0	15	2	S24159	leukocyte elastase
13	13	50.0	16	2	A60551	leukocyte elastase

14	13	50.0	16	2	PH0137	T-cell receptor be
15	13	50.0	19	2	S77993	cytochrome-c oxida
16	13	50.0	20	2	B53875	creatine kinase (E
17	13	50.0	20	2	A53875	creatine kinase (E
18	13	50.0	20	2	PQ0688	photosystem I 14.0
19	13	50.0	20	2	PQ0687	photosystem I 14.1
20	13	50.0	20	2	S78759	ribosomal protein
21	12	46.2	4	2	PT0712	T-cell receptor be
22	12	46.2	9	2	A31576	xylose isomerase (
23	12	46.2	10	1	ECLQ4M	tachykinin IV - mi
24	12	46.2	10	2	S43625	cytochrome-c oxida
25	12	46.2	10	2	PH1592	Ig H chain V-D-J r
26	12	46.2	11	2	S65395	chemical-sense-rel
27	12	46.2	13	2	I51905	collecting duct wa
28	12	46.2	14	2	S48685	extension protein
29	12	46.2	14	2	PS0258	38K protein 3228 -
30	12	46.2	15	2	PA0059	protein QF200021 -
31	12	46.2	15	2	A60221	apolipoprotein A-I
32	12	46.2	15	2	B32800	hypothetical prote
33	12	46.2	15	2	S30608	translation elonga
34	12	46.2	15	2	S08301	epidermal growth f
35	12	46.2	15	2	C56979	collagen alpha 1(I
36	12	46.2	16	2	A39109	hypothetical prote
37	12	46.2	16	2	PC1299	subtilisin (EC 3.4
38	12	46.2	16	2	S33589	beta-crystallin A4
39	12	46.2	17	2	A60317	glucagon-like pept
40	12	46.2	17	2	A49635	Golli-mbp - human
41	12	46.2	17	2	S57555	T cell receptor V-
42	12	46.2	17	2	A46218	ubiquinol-cytochro
43	12	46.2	18	2	I51427	hemoglobin alpha c
44	12	46.2	18	2	S55501	thrombospondin pre
45	12	46.2	18	2	A60277	pilin - Vibrio par
46	12	46.2	18	2	F27480	hydrogenase (EC 1.
47	12	46.2	19	2	S20289	cytochrome-c oxida
48	12	46.2	19	2	A48400	phosphocarrier pro
49	12	46.2	19	2	S63489	dissimilatory sulf
50	12	46.2	20	2	B37520	glutathione transf
51	12	46.2	20	2	S29099	glutathione transf
52	12	46.2	20	2	S71869	glutathione transf
53	12	46.2	20	2	A14344	alanine transamina
54	12	46.2	20	2	PH0111	style glycoprotein
55	12	46.2	20	2	S33787	pancreatic elastas
56	12	46.2	20	2	B48400	phosphocarrier pro
57	12	46.2	20	2	PS0028	flagellar motor sw
58	12	46.2	20	2	S63490	dissimilatory sulf
59	12	46.2	20	2	A20569	C-reactive protein
60	12	46.2	20	2	S27350	lysophospholipase
61	12	46.2	20	2	PQ0537	arylhydroxamic aci
62	12	46.2	20	2	A60897	class I histocompa
63	12	46.2	20	2	S21244	H+-transporting tw
64	11	42.3	6	2	S71349	beta-crystallin B2
65	11	42.3	6	4	S15596	orf 3 rara 5'-regi
66	11	42.3	8	2	PT0311	Ig heavy chain CRD
67	11	42.3	9	2	S07241	litorin - Rohde's
68	11	42.3	9	2	S10920	venom protein HR-3
69	11	42.3	10	2	A61289	streptopain (EC 3.
70	11	42.3	10	2	A46491	C3 homolog HX - in

ALIGNMENTS

RESULT 1
S65730
hemoglobin, extracellular, component - earthworm (Lumbricus terrestris)
(fragment)
C;Species: Lumbricus terrestris (common earthworm)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S65730
R;Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
Biochim. Biophys. Acta 1292, 273-280, 1996
A;Title: Characterization of the constituent polypeptides of the extracellular
hemoglobin from Lumbricus terrestris: heterogeneity and discovery of a new
linker chain L4.
A;Reference number: S65721; MUID:96176855; PMID:8597573
A;Accession: S65730
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <FUS>

  Query Match 65.4%; Score 17; DB 2; Length 12;
  Best Local Similarity 50.0%; Pred. No. 1e+02;
  Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 PXAXXH 6
              | |  |
Db          3 PSARDH 8
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Search completed: April 5, 2004, 09:05:41
Job time : 29 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 5, 2004, 09:01:52 ; Search time 20 Seconds
(without alignments)
33.667 Million cell updates/sec

Title: US-09-972-772A-16
Perfect score: 26
Sequence: 1 PXAXXHA 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 3885

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	65.4	12	2	S65730	hemoglobin, extrac
2	16	61.5	15	2	S36893	ribosomal protein
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4	15	57.7	20	2	PH0110	style glycoprotein
5	14	53.8	14	2	PL0142	carbon-monoxide de
6	14	53.8	15	2	B45133	casein kinase II (
7	14	53.8	20	2	S15861	estrogen receptor
8	13	50.0	5	2	JN0860	peptidyl-dipeptida
9	13	50.0	13	1	NTKN2G	alpha-conotoxin GI
10	13	50.0	14	2	S22236	lipoxygenase (EC 1
11	13	50.0	15	1	NTKNAG	alpha-conotoxin GI
12	13	50.0	15	2	S24159	leukocyte elastase
13	13	50.0	16	2	A60551	leukocyte elastase

14	13	50.0	16	2	PH0137	T-cell receptor be
15	13	50.0	19	2	S77993	cytochrome-c oxida
16	13	50.0	20	2	B53875	creatine kinase (E
17	13	50.0	20	2	A53875	creatine kinase (E
18	13	50.0	20	2	PQ0688	photosystem I 14.0
19	13	50.0	20	2	PQ0687	photosystem I 14.1
20	13	50.0	20	2	S78759	ribosomal protein
21	12	46.2	4	2	PT0712	T-cell receptor be
22	12	46.2	9	2	A31576	xylose isomerase (
23	12	46.2	10	1	ECLQ4M	tachykinin IV - mi
24	12	46.2	10	2	S43625	cytochrome-c oxida
25	12	46.2	10	2	PH1592	Ig H chain V-D-J r
26	12	46.2	11	2	S65395	chemical-sense-rel
27	12	46.2	13	2	I51905	collecting duct wa
28	12	46.2	14	2	S48685	extension protein
29	12	46.2	14	2	PS0258	38K protein 3228 -
30	12	46.2	15	2	PA0059	protein QF200021 -
31	12	46.2	15	2	A60221	apolipoprotein A-I
32	12	46.2	15	2	B32800	hypothetical prote
33	12	46.2	15	2	S30608	translation elonga
34	12	46.2	15	2	S08301	epidermal growth f
35	12	46.2	15	2	C56979	collagen alpha 1(I
36	12	46.2	16	2	A39109	hypothetical prote
37	12	46.2	16	2	PC1299	subtilisin (EC 3.4
38	12	46.2	16	2	S33589	beta-crystallin A4
39	12	46.2	17	2	A60317	glucagon-like pept
40	12	46.2	17	2	A49635	Golli-mbp - human
41	12	46.2	17	2	S57555	T cell receptor V-
42	12	46.2	17	2	A46218	ubiquinol-cytochro
43	12	46.2	18	2	I51427	hemoglobin alpha c
44	12	46.2	18	2	S55501	thrombospondin pre
45	12	46.2	18	2	A60277	pilin - Vibrio par
46	12	46.2	18	2	F27480	hydrogenase (EC 1.
47	12	46.2	19	2	S20289	cytochrome-c oxida
48	12	46.2	19	2	A48400	phosphocarrier pro
49	12	46.2	19	2	S63489	dissimilatory sulf
50	12	46.2	20	2	B37520	glutathione transf
51	12	46.2	20	2	S29099	glutathione transf
52	12	46.2	20	2	S71869	glutathione transf
53	12	46.2	20	2	A14344	alanine transamina
54	12	46.2	20	2	PH0111	style glycoprotein
55	12	46.2	20	2	S33787	pancreatic elastas
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58	12	46.2	20	2	S63490	dissimilatory sulf
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60	12	46.2	20	2	S27350	lysophospholipase
61	12	46.2	20	2	PQ0537	arylhydroxamic aci
62	12	46.2	20	2	A60897	class I histocompa
63	12	46.2	20	2	S21244	H+-transporting tw
64	11	42.3	6	2	S71349	beta-crystallin B2
65	11	42.3	6	4	S15596	orf 3 rara 5'-regi
66	11	42.3	8	2	PT0311	Ig heavy chain CRD
67	11	42.3	9	2	S07241	litorin - Rohde's
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69	11	42.3	10	2	A61289	streptopain (EC 3.
70	11	42.3	10	2	A46491	C3 homolog HX - in

ALIGNMENTS

RESULT 1
S65730
hemoglobin, extracellular, component - earthworm (Lumbricus terrestris)
(fragment)
C;Species: Lumbricus terrestris (common earthworm)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S65730
R;Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
Biochim. Biophys. Acta 1292, 273-280, 1996
A;Title: Characterization of the constituent polypeptides of the extracellular hemoglobin from Lumbricus terrestris: heterogeneity and discovery of a new linker chain L4.
A;Reference number: S65721; MUID:96176855; PMID:8597573
A;Accession: S65730
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <FUS>

  Query Match 65.4%; Score 17; DB 2; Length 12;
  Best Local Similarity 50.0%; Pred. No. 1e+02;
  Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 PXAXXH 6
              | |  |
Db          3 PSARDH 8
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Search completed: April 5, 2004, 09:05:41
Job time : 29 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 5, 2004, 09:05:28 ; Search time 40 Seconds
(without alignments)
45.955 Million cell updates/sec

Title: US-09-972-772A-16
Perfect score: 26
Sequence: 1 PXAXXHA 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1071436 seqs, 262597696 residues

Total number of hits satisfying chosen parameters: 205293

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA:*
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17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	21	80.8	17	15	US-10-289-009-14	Sequence 14, Appl
2	21	80.8	18	15	US-10-289-009-13	Sequence 13, Appl
3	21	80.8	19	15	US-10-289-009-12	Sequence 12, Appl
4	20	76.9	7	9	US-09-972-772-16	Sequence 16, Appl
5	20	76.9	7	9	US-09-972-772-17	Sequence 17, Appl
6	20	76.9	7	13	US-10-001-945-16	Sequence 16, Appl
7	20	76.9	7	13	US-10-001-945-17	Sequence 17, Appl
8	20	76.9	7	14	US-10-138-935-16	Sequence 16, Appl
9	20	76.9	7	14	US-10-138-935-17	Sequence 17, Appl
10	19	73.1	10	10	US-09-572-404B-2288	Sequence 2288, Ap
11	19	73.1	12	14	US-10-286-457-222	Sequence 222, App
12	19	73.1	20	12	US-10-430-685-80	Sequence 80, Appl
13	18	69.2	10	9	US-09-753-126-113	Sequence 113, App
14	18	69.2	10	10	US-09-896-896A-77	Sequence 77, Appl
15	18	69.2	10	10	US-09-572-404B-3546	Sequence 3546, Ap
16	18	69.2	10	15	US-10-330-697-113	Sequence 113, App
17	18	69.2	11	10	US-09-974-879-425	Sequence 425, App
18	18	69.2	11	10	US-09-305-736-425	Sequence 425, App
19	18	69.2	11	11	US-09-818-683-425	Sequence 425, App
20	18	69.2	11	12	US-10-621-401-425	Sequence 425, App
21	18	69.2	13	12	US-10-433-561-150	Sequence 150, App
22	18	69.2	14	10	US-09-273-217-3	Sequence 3, Appli
23	18	69.2	14	12	US-10-433-561-151	Sequence 151, App
24	18	69.2	15	9	US-09-821-883-16	Sequence 16, Appl
25	18	69.2	20	14	US-10-094-401-137	Sequence 137, App
26	18	69.2	20	14	US-10-280-066-354	Sequence 354, App
27	18	69.2	20	15	US-10-462-262-105	Sequence 105, App
28	17	65.4	9	10	US-09-799-250-256	Sequence 256, App
29	17	65.4	9	10	US-09-799-250-341	Sequence 341, App
30	17	65.4	9	10	US-09-799-250-439	Sequence 439, App
31	17	65.4	9	10	US-09-799-250-550	Sequence 550, App
32	17	65.4	9	10	US-09-799-250-660	Sequence 660, App
33	17	65.4	10	10	US-09-799-250-82	Sequence 82, Appl
34	17	65.4	10	10	US-09-799-250-176	Sequence 176, App
35	17	65.4	10	10	US-09-799-250-290	Sequence 290, App
36	17	65.4	10	10	US-09-799-250-310	Sequence 310, App
37	17	65.4	10	10	US-09-799-250-376	Sequence 376, App
38	17	65.4	10	10	US-09-799-250-389	Sequence 389, App
39	17	65.4	10	10	US-09-799-250-406	Sequence 406, App
40	17	65.4	10	10	US-09-799-250-589	Sequence 589, App
41	17	65.4	10	10	US-09-799-250-598	Sequence 598, App
42	17	65.4	10	10	US-09-799-250-709	Sequence 709, App
43	17	65.4	10	10	US-09-799-250-713	Sequence 713, App
44	17	65.4	12	10	US-09-954-385-403	Sequence 403, App
45	17	65.4	12	14	US-10-254-446A-220	Sequence 220, App
46	17	65.4	12	14	US-10-286-457-184	Sequence 184, App
47	17	65.4	13	9	US-09-994-485-21	Sequence 21, Appl
48	17	65.4	13	9	US-09-832-292-15	Sequence 15, Appl
49	17	65.4	14	14	US-10-185-050-222	Sequence 222, App
50	17	65.4	15	8	US-08-955-373-7	Sequence 7, Appli
51	17	65.4	15	10	US-09-964-821B-27	Sequence 27, Appl
52	17	65.4	15	14	US-10-225-567A-1619	Sequence 1619, Ap
53	17	65.4	15	14	US-10-268-332-27	Sequence 27, Appl
54	17	65.4	16	8	US-08-955-373-8	Sequence 8, Appli
55	17	65.4	17	9	US-09-864-761-42256	Sequence 42256, A
56	17	65.4	18	10	US-09-983-802-376	Sequence 376, App

ALIGNMENTS

RESULT 1
US-10-289-009-14
; Sequence 14, Application US/10289009
; Publication No. US20030228700A1
; GENERAL INFORMATION:
; APPLICANT: Peters, Eric C.
; APPLICANT: Brock, Ansgar
; APPLICANT: Ericson, Christer
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Labeling Reagent and Methods of Use
; FILE REFERENCE: 021288-000230US
; CURRENT APPLICATION NUMBER: US/10/289,009
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US 60/332,988
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/385,835
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/410,382
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:equine
; OTHER INFORMATION: myoglobin tryptic polypeptide #13
US-10-289-009-14

Query Match 80.8%; Score 21; DB 15; Length 17;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 PXAXXHA 7
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Db          9 PLAQSHA 15
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RESULT 4
US-09-972-772-16
; Sequence 16, Application US/09972772
; Publication No. US20020193298A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Gary L.
; APPLICANT: Self, Christopher
; APPLICANT: Lee, Lily
; APPLICANT: Cook, Charles M.
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS
; FILE REFERENCE: PPI-106CP
; CURRENT APPLICATION NUMBER: US/09/972,772

; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 09/704,251
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motifs
; NAME/KEY: VARIANT
; LOCATION: 2
; OTHER INFORMATION: Xaa at position 2 represents L-cyclohexylalanine
; NAME/KEY: VARIANT
; LOCATION: 4
; OTHER INFORMATION: Xaa at position 4 represents L-a-aminobutyryl
; NAME/KEY: VARIANT
; LOCATION: 5
; OTHER INFORMATION: Xaa at position 5 represents methylated cysteine
US-09-972-772-16

Query Match 76.9%; Score 20; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 PXAXXHA 7
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; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2288
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in MEOX2 OR MOX2 OR GAX at 99-108 and may interact with
; OTHER INFORMATION: Sequence 2287 in this patent.
US-09-572-404B-2288

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Qy          1 PXAXXHA 7
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Db          2 PSAARHS 8


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Job time : 45 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 5, 2004, 09:02:43 ; Search time 23 Seconds
(without alignments)
15.712 Million cell updates/sec

Title: US-09-972-772A-16
Perfect score: 26
Sequence: 1 PXAXXHA 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 173459

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	21	80.8	11	5	PCT-US91-09152-16	Sequence 16, Appl
2	20	76.9	7	4	US-09-704-251-16	Sequence 16, Appl
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5	18	69.2	9	2	US-08-340-283-84	Sequence 84, Appl
6	18	69.2	11	3	US-08-893-526A-16	Sequence 16, Appl
7	18	69.2	16	2	US-08-528-057-12	Sequence 12, Appl
8	17	65.4	6	1	US-08-406-347A-20	Sequence 20, Appl
9	17	65.4	11	1	US-08-211-942-18	Sequence 18, Appl
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11	17	65.4	14	3	US-09-188-579-98	Sequence 98, Appl

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13	17	65.4	14	4	US-09-721-362-98	Sequence 98, Appl
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15	17	65.4	18	1	US-08-423-399B-15	Sequence 15, Appl
16	17	65.4	18	2	US-09-017-205-44	Sequence 44, Appl
17	17	65.4	18	4	US-09-227-357-376	Sequence 376, App
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41	16	61.5	16	4	US-09-187-789-77	Sequence 77, Appl
42	16	61.5	16	4	US-09-139-600-3	Sequence 3, Appli
43	16	61.5	16	4	US-09-205-258-1064	Sequence 1064, Ap
44	16	61.5	16	4	US-09-658-517C-18	Sequence 18, Appl
45	16	61.5	17	1	US-07-591-988B-1	Sequence 1, Appli
46	16	61.5	17	1	US-07-591-988B-2	Sequence 2, Appli
47	16	61.5	17	1	US-07-591-988B-4	Sequence 4, Appli
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49	16	61.5	17	1	US-08-164-618-3	Sequence 3, Appli
50	16	61.5	17	1	US-08-006-037-1	Sequence 1, Appli
51	16	61.5	17	1	US-08-006-037-2	Sequence 2, Appli
52	16	61.5	17	1	US-08-006-037-4	Sequence 4, Appli
53	16	61.5	17	2	US-08-614-377A-11	Sequence 11, Appl
54	16	61.5	17	3	US-09-142-648B-11	Sequence 11, Appl
55	16	61.5	18	3	US-08-812-121-16	Sequence 16, Appl
56	16	61.5	18	4	US-09-403-672-16	Sequence 16, Appl
57	16	61.5	20	1	US-08-221-583-15	Sequence 15, Appl
58	16	61.5	20	3	US-08-752-892-3	Sequence 3, Appli
59	16	61.5	20	5	PCT-US95-04018-15	Sequence 15, Appl
60	16	61.5	20	5	PCT-US95-06726-4	Sequence 4, Appli
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62	15	57.7	7	4	US-09-183-861-57	Sequence 57, Appl
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64	15	57.7	7	4	US-09-551-974A-57	Sequence 57, Appl
65	15	57.7	7	4	US-09-565-501A-57	Sequence 57, Appl
66	15	57.7	7	4	US-09-639-206A-57	Sequence 57, Appl
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68	15	57.7	9	2	US-08-340-283-125	Sequence 125, App

69	15	57.7	9	3	US-09-101-167-14	Sequence 14, Appl
70	15	57.7	10	4	US-09-254-776B-70	Sequence 70, Appl
71	15	57.7	10	4	US-08-234-784B-76	Sequence 76, Appl
72	15	57.7	11	3	US-08-750-419A-21	Sequence 21, Appl
73	15	57.7	11	4	US-09-811-672-18	Sequence 18, Appl
74	15	57.7	13	3	US-08-750-419A-22	Sequence 22, Appl
75	15	57.7	13	3	US-08-939-853A-11	Sequence 11, Appl
76	15	57.7	13	3	US-08-786-284A-4	Sequence 4, Appli
77	15	57.7	13	4	US-09-811-672-19	Sequence 19, Appl
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88	15	57.7	15	2	US-08-723-415B-17	Sequence 17, Appl
89	15	57.7	15	2	US-08-605-002A-1	Sequence 1, Appli
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92	15	57.7	15	3	US-08-750-419A-18	Sequence 18, Appl
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103	15	57.7	15	5	PCT-US94-10529-1	Sequence 1, Appli
104	15	57.7	16	2	US-08-679-405-10	Sequence 10, Appl
105	15	57.7	16	2	US-08-950-449A-17	Sequence 17, Appl
106	15	57.7	16	2	US-08-842-799-10	Sequence 10, Appl
107	15	57.7	16	5	PCT-US96-11458-10	Sequence 10, Appl
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109	15	57.7	17	1	US-07-591-988B-5	Sequence 5, Appli
110	15	57.7	17	1	US-08-164-618-4	Sequence 4, Appli
111	15	57.7	17	1	US-08-006-037-3	Sequence 3, Appli
112	15	57.7	17	1	US-08-006-037-5	Sequence 5, Appli
113	15	57.7	17	3	US-08-750-419A-19	Sequence 19, Appl
114	15	57.7	17	4	US-09-205-258-846	Sequence 846, App
115	15	57.7	17	4	US-09-811-672-16	Sequence 16, Appl
116	15	57.7	18	3	US-08-750-419A-7	Sequence 7, Appli
117	15	57.7	18	4	US-09-811-672-7	Sequence 7, Appli
118	15	57.7	19	3	US-08-882-046-11	Sequence 11, Appl
119	15	57.7	20	1	US-07-718-274A-20	Sequence 20, Appl
120	15	57.7	20	1	US-08-149-106-20	Sequence 20, Appl
121	15	57.7	20	1	US-08-298-021-20	Sequence 20, Appl
122	15	57.7	20	1	US-08-440-861-40	Sequence 40, Appl
123	15	57.7	20	3	US-09-230-421-8	Sequence 8, Appli
124	15	57.7	20	3	US-09-162-934-13	Sequence 13, Appl
125	14	53.8	7	4	US-09-183-861-58	Sequence 58, Appl

ALIGNMENTS

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RESULT 1
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; Sequence 16, Application PC/TUS9109152
;  GENERAL INFORMATION:
;    APPLICANT:  Kubiak, Teresa M.
;    APPLICANT:  Sharma, Satish K.
;    TITLE OF INVENTION:  Fusion Polypeptides
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Upjohn Company - Corp. Patents & Trademarks
;      STREET:  301 Henrietta Street
;      CITY:  Kalamazoo
;      STATE:  Michigan
;      COUNTRY:  USA
;      ZIP:  49001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  diskette (3M 3.5, DS double side 1.0 MB)
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US91/09152
;      FILING DATE:  19911212
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US07/626,727
;      FILING DATE:  13/12/90
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US07/614,170
;      FILING DATE:  14/11/90
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US90/02923
;      FILING DATE:  30/05/90
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US07/368,231
;      FILING DATE:  16/06/89
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US07/506,605
;      FILING DATE:  09/04/90
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33229
;      REFERENCE/DOCKET NUMBER:  4595
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  616  385  5210
;      TELEFAX:  616  385  6897
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
PCT-US91-09152-16

  Query Match             80.8%;  Score 21;  DB 5;  Length 11;
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Best Local Similarity 57.1%; Pred. No. 21;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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              | |  ||
Db          3 PHAHAHA 9
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RESULT 2
US-09-704-251-16
; Sequence 16, Application US/09704251
; Patent No. 6548477
; GENERAL INFORMATION:
; APPLICANT: Olson, Gary L.
; APPLICANT: Self, Christopher
; APPLICANT: Lee, Lily
; APPLICANT: Cook, Charles M.
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS
; FILE REFERENCE: PPI-106
; CURRENT APPLICATION NUMBER: US/09/704,251
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motifs
; OTHER INFORMATION: Xaa at position 2 represents L-cyclohexylalanine
; OTHER INFORMATION: Xaa at position 4 represents L-a-aminobutyryl
; OTHER INFORMATION: Xaa at position 5 represents methylated cysteine
US-09-704-251-16

Query Match 76.9%; Score 20; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 PXAXXHA 7
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RESULT 4
US-08-340-283-22
; Sequence 22, Application US/08340283
; Patent No. 5861318
; GENERAL INFORMATION:
; APPLICANT: Elhammer, Ake P.
; TITLE OF INVENTION: A SCINTILLATION PROXIMITY ASSAY FOR
; TITLE OF INVENTION: N-ACETYLGALACTOSAMINYLTRANSFERASE ACTIVITY
; NUMBER OF SEQUENCES: 205
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia and Upjohn, Inc., Intellect. Prop. Law
; ADDRESSEE: (1920-32-1)

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;       STREET:  301 Henrietta Street
;       CITY:  Kalamazoo
;       STATE:  Michigan
;       COUNTRY:  U.S.A.
;       ZIP:  49001
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/340,283
;       FILING DATE:
;       CLASSIFICATION:  436
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Wootton, Thomas A.
;       REGISTRATION NUMBER:  35,004
;       REFERENCE/DOCKET NUMBER:  4828
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (616) 385-7914
;       TELEFAX:  (616) 385-6897
;       TELEX:  224401
;   INFORMATION FOR SEQ ID NO:  22:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  9 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FRAGMENT TYPE:  N-terminal
US-08-340-283-22

  Query Match             69.2%;  Score 18;  DB 2;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 3e+05;
  Matches    3;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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Db          2 PHATSH 7


Search completed: April  5, 2004, 09:06:16
Job time : 31 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 5, 2004, 08:57:37 ; Search time 53 Seconds
(without alignments)
37.318 Million cell updates/sec

Title: US-09-972-772A-16
Perfect score: 26
Sequence: 1 PXAXXHA 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 506618

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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3	21	80.8	13	6	ABU14453	Abu14453 hFSH pept
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5	21	80.8	13	6	ABU14449	Abu14449 hFSH pept
6	21	80.8	13	6	ABU14448	Abu14448 hFSH pept
7	21	80.8	13	6	ABU14450	Abu14450 hFSH pept
8	21	80.8	17	6	ADA74731	Ada74731 Tryptical
9	21	80.8	18	6	ADA74730	Ada74730 Tryptical

10	21	80.8	19	2	AAW16890	Aaw16890 Helicobac
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17	19	73.1	7	5	AAE26707	Aae26707 Matrix me
18	19	73.1	7	7	AAE39186	Aae39186 Angiogene
19	19	73.1	7	7	AAE39185	Aae39185 Angiogene
20	19	73.1	10	4	AAG96094	Aag96094 Human com
21	19	73.1	12	7	ADC44494	Adc44494 Endotheli
22	19	73.1	16	4	AAB46623	Aab46623 HIV-1 Tat
23	19	73.1	20	5	AAU99411	Aau99411 Human ECS
24	18	69.2	9	2	AAW06997	Aaw06997 Synthetic
25	18	69.2	9	2	AAW07059	Aaw07059 Synthetic
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32	18	69.2	10	7	ADE69215	Ade69215 Human 161
33	18	69.2	10	7	ADE69783	Ade69783 Human 161
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38	18	69.2	10	7	ADE69443	Ade69443 Human 161
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40	18	69.2	11	6	ABO14257	Abo14257 Novel hum
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113	17	65.4	11	6	ADB20733	Adb20733 MRP1 base
114	17	65.4	11	7	ADB87822	Adb87822 Human UGT
115	17	65.4	11	7	ADB96805	Adb96805 Human UGT
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117	17	65.4	12	3	AAY92993	Aay92993 Transform
118	17	65.4	12	5	AAU87878	Aau87878 PDZ domai
119	17	65.4	12	6	ABR75367	Abr75367 Biologica
120	17	65.4	12	6	ABU14214	Abu14214 N-termina
121	17	65.4	12	6	ABU14216	Abu14216 N-termina
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123	17	65.4	12	6	ABU14399	Abu14399 C- or N-t

ALIGNMENTS

RESULT 1
AAR25097
ID AAR25097 standard; protein; 11 AA.
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AC AAR25097;
XX
DT 25-MAR-2003 (revised)
DT 23-DEC-1992 (first entry)
XX
DE bGRF prodrug analogue 16.
XX
KW Bovine growth hormone releasing factor; dipeptidylpeptidase IV; DPP IV;
KW purification; medicament.
XX
OS Synthetic.
XX
PN WO9210576-A1.
XX
PD 25-JUN-1992.
XX
PF 12-DEC-1991; 91WO-US009152.
XX
PR 13-DEC-1990; 90US-00626727.
XX
PA (UPJO) UPJOHN CO.
XX
PI Kubiak TM, Sharma SK;
XX
DR WPI; 1992-234631/28.
XX
PT Non-naturally occurring fusion protein prodrug - is cleaved in=vivo by
PT host di:peptidyl peptides IV to achieve sustained release, e.g. of growth
PT hormone.
XX
PS Disclosure; Page 38; 55pp; English.
XX
CC The sequences given in AAR25082-109 and AAR25247-62 are N-terminally
CC extended bovine growth hormone releasing factor (bGRF) prodrug analogues.
CC The N-terminal extension is cleavable by dipeptidylpeptidase IV (DPP IV).
CC Exposure of these bGRF prodrug analogues to DPP IV results in their
CC conversion to desirable proteins. These prodrugs are converted to
CC prodrugs using a patients endogenous DPP IV, thereby achieving sustained
CC presence of the active drug in a patient and reducing the frequency of
CC administration. These proteins are useful in purification methods were
CC the N-terminal extension facilitates purification. They may also be used
CC to prepare a medicament. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

  Query Match   80.8%; Score 21; DB 2; Length 11;
  Best Local Similarity   57.1%; Pred. No. 87;
  Matches   4; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   1 PXAXXHA 7

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                | |  ||
Db          3 PHAHAHA 9


RESULT 2
ABU14452
ID   ABU14452 standard; peptide; 13 AA.
XX
AC   ABU14452;
XX
DT   12-MAR-2003  (first entry)
XX
DE   hFSH peptide #15 used in multi-building block scan.
XX
KW   Biomolecule detection; pixel array; micro-array support;
KW   molecule binding; binding molecule; support surface; surface patch;
KW   high density arraying; enzyme-linked-assay; multi-building block scan;
KW   human follicle-stimulating hormone; hFSH.
XX
OS   Homo sapiens.
XX
PN   WO200266984-A2.
XX
PD   29-AUG-2002.
XX
PF   15-FEB-2002; 2002WO-NL000097.
XX
PR   16-FEB-2001; 2001EP-00200551.
XX
PA   (PEPS-) PEPSCAN SYSTEMS BV.
XX
PI   Puijk WC,  Van Dijk E,  Slootstra JW;
XX
DR   WPI; 2003-103161/09.
XX
PT   Novel support used for micro-arrays and its use in detection of (bio)
PT   molecules.
XX
PS   Example 4; Fig 7C; 41pp; English.
XX
CC   The present invention relates to a method for the detection of
CC   biomolecules in pixel arrays and the supports used for the micro-arrays.
CC   The novel supports for the micro-arrays are suitable for determining the
CC   binding of a first member molecule within a library of spots of tentative
CC   first member binding molecules with a second member binding molecule. The
CC   support is provided with a support surface where surface patches are
CC   interspersed with surface areas that are materially distinct from the
CC   patches. The support and method of the invention are useful for
CC   identifying or obtaining a synthetic molecule comprising a binding site,
CC   or a binding molecule capable of binding to a binding site. The molecule
CC   is useful for interfering with, or effecting binding to a binding
CC   molecule. The novel support for a micro-array and the method provide high
CC   density arraying (testing many binding events in one go) and enzyme-
CC   linked-assays (very sensitive) allowing the detection of more binding
CC   pairs more rapidly. ABU14438-ABU14473 represent human follicle-
CC   stimulating hormone (hFSH) peptides used in a multi-building block scan
CC   in the method of the present invention
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XX
SQ Sequence 13 AA;

  Query Match 80.8%; Score 21; DB 6; Length 13;
  Best Local Similarity 57.1%; Pred. No. 1e+02;
  Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 PXAXXHA 7
              | |  ||
Db          2 PGAAHHA 8
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Search completed: April 5, 2004, 09:04:10
Job time : 79 secs